

## (12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau(43) International Publication Date  
7 December 2000 (07.12.2000)

PCT

(10) International Publication Number  
WO 00/73467 A1(51) International Patent Classification<sup>7</sup>: C12N 15/52,  
15/62, 15/11, 5/10, 9/14, C07K 16/40, G01N 33/50,  
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(21) International Application Number: PCT/US00/14719

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(22) International Filing Date: 25 May 2000 (25.05.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
60/136,620 27 May 1999 (27.05.1999) US  
09/579,181 25 May 2000 (25.05.2000) US(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE,  
DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU,  
ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,  
LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ,  
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,  
TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.(63) Related by continuation (CON) or continuation-in-part  
(CIP) to earlier application:  
US 60/136,620 (CON)  
Filed on 27 May 1999 (27.05.1999)(84) Designated States (*regional*): ARIPO patent (GH, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian  
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European  
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,  
IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG,  
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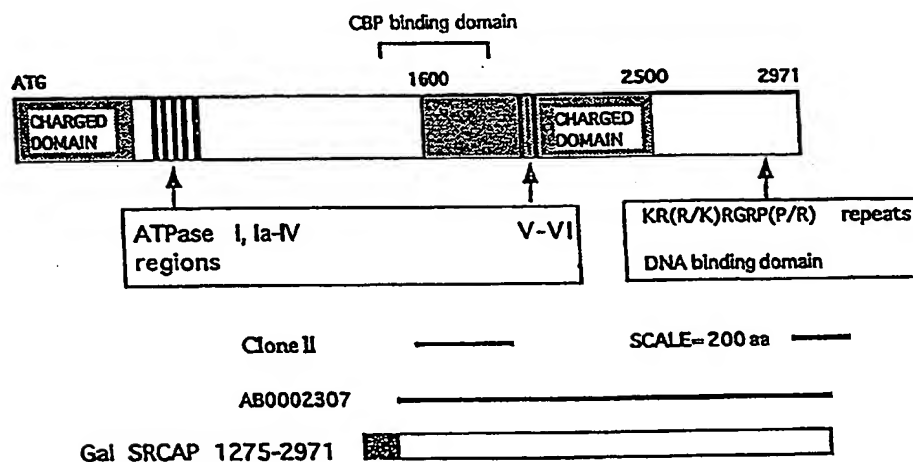
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Published:

(75) Inventors/Applicants (for US only): CHRIVIA, John — With international search report.

[Continued on next page]

(54) Title: SNF2 RELATED CBP ACTIVATOR PROTEIN (SRCAP)



(57) Abstract: A protein, SRCAP, is provided. The protein is capable of co-activating CREB binding protein (CBP) mediated transcription, as well as activating transcription without CBP. SRCAP is a Snf2 family member. As such, it has ATPase activity. Fragments of SRCAP are also provided, as are polynucleotides encoding SRCAP and its fragments. Antibodies that bind to SRCAP are also provided. These compositions are useful for enhancing transcription in cells and patients. The compositions are also useful for reducing transcription in cells and patients.



— Before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments.

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

## SNF2 RELATED CBP ACTIVATOR PROTEIN (SRCAP)

This application claims the benefit of U.S. Provisional Application No. 60/136,620, filed May 27, 1999, incorporated in its entirety herein by reference.

This invention was made with Government support under National Institutes of Health Grant No. DK52231. The Government has certain rights in the invention.

5 Background of the Invention

## (1) Field of the Invention

The present invention generally relates to regulation of transcription factors. More specifically, the invention relates to a novel SNF2/SWI2 protein family member, SRCAP, that is capable of activating transcription directly as well as interacting with CREB binding protein (CBP) to enhance the ability of CBP to activate transcription.

## 10 (2) Description of the Related Art

Transcription factors are well known as proteins that bind to regulatory regions of genes and other proteins to modulate transcription of the genes. Examples of transcription factors relevant to this invention include CREB, c-jun, c-myc, MyoD, E2F1, YY1, TBP, TFIIB, and RNAP II. The action of these transcription factors is affected by co-activators, notably CREB binding protein (CBP).

15 CBP is a histone acetyltransferase capable of acetylating not only histones but also several transcription factors such as GATA-1 and p53 (Boyes et al., 1998, *Nature* 396, 594-598; Hung et al., 1999, *Cell Biol.* 19, 3496-3505; Webster et al., 1999, *Mol. Cell. Biol.* 19, 3485-3495). CBP also binds to several proteins that also function as histone acetyltransferases (P/CAF, p/CIP and the p160 co-activators such as SRC-1).

20 Precisely how CBP interacts with these co-activators and other cellular factors to activate transcription has not been completely elucidated. The notion that CBP interacts with a specific subset of factors at different promoters was first suggested by the work of Korzus et al., 1998, *Science* 279, 703-707. These authors showed that CBP in conjunction with P/CIP, SRC-1 and P/CAF was required for activation of transcription of a RARE reporter gene by the retinoic acid receptor, whereas only CBP, P/CAF and p/CIP were needed for activation of a CRE reporter gene by CREB and only CBP and P/CAF are required for transcription of a

GAS-reporter gene by STAT-1. In addition the HAT activity of each of these co-activators was not needed at each promoter. For example, with the RARE- reporter gene, despite the fact that the pCIP-P/CAF-SRC-1-CBP complex was needed for activation of transcription, only the HAT activity of P/CAF was needed, whereas transcription of the CRE-reporter by the CBP-P/CAF-pCIP complex required the HAT activity of CBP not p/CAF. Thus, the specific transcription factors which CBP binds determine not only the requirement for specific co-activators but whether their HAT activity is also needed. The requirement for a specific HAT function may also be altered depending on what signaling pathways activate transcription. Xu et al. (1998, *Nature* 395, 301-306) have reported that forskolin activation of Pit1 mediated transcription requires the HAT function of CBP whereas insulin activation of Pit1 mediated transcription does not.

Why different HAT activities are needed is unclear but CBP, P/CAF and p/CIP have been shown to have different substrate specificities (Perissi et al., 1999, *Proc. Natl. Acad. Sci. U.S.A.* 96, 3652-3657) suggesting they acetylate a different subset of proteins. The possibility that substrate specificity of these proteins may be regulated is illustrated by the work of Perissi et al. (*Id.*) who reported that binding of p/CIP to CBP changes the substrate specificity of CBP. Repression of the HAT activity of CBP by the adenoviral 12S E1A protein has been reported by several laboratories and occurs through E1A contacts with the HAT domain of CBP (Charkravati et al., 1999, *Cell* 96, 393-403, reviewed in Goldman et al., 1997, *Recent Prog. Horm. Res.* 52, 103-120). In contrast to these findings, recent work by Ait-Si Ali et al. (1998, *Nature* 396, 184-186) indicates that in some circumstances E1A can stimulate the HAT activity of CBP.

The activity of several kinases has been shown to regulate CBP function. The NGF stimulated kinase, p42/44<sup>MAPK</sup>, activates CBP mediated transcription by a phosphorylation event which is blocked by the MAPK inhibitor PD 98059. p42/44<sup>MAPK</sup> directly associates with CBP and can phosphorylate CBP *in vitro* (Liu et al., 1999, *Neuroreport* 10, 1239-1243). Studies have also demonstrated the cyclin E-cyclin dependent kinase 2 (cdk2) complex binds CBP and mediates hyperphosphorylation of CBP at the G1/S boundary (Ait-Si Ali et al., *supra*). Inhibition of cyclin E-Cdk2 by the cyclin dependent kinase inhibitor p21, results in the activation of NF- $\kappa$ B mediated transcription (Perkins et al., 1997, *Science* 275, 523-527). The binding of the kinase pp90<sup>RSK</sup> to CBP has different effects depending on the signaling pathway. pp90<sup>RSK</sup>-CBP interaction is needed for insulin stimulated transcription, and blocks the ability of CBP to function as a co-activator for cAMP-mediated transcription. The activity of pp90<sup>RSK</sup> can be mimicked by a kinase defective mutant, indicating association of pp90<sup>RSK</sup> with CBP is enough to alter its function (Nakajima et al., 1996, *Cell* 86, 465-474).



Other studies have also demonstrated that protein kinase A and CAM kinase II and IV positively modulate the ability of specific domains within CBP to activate transcription. However, the precise mechanism by which this occurs has not been delineated (Swope et al., 1996, *J. Biol. Chem.* 271, 28138-28145; Liu et al., 1998, *J. Biol. Chem.* 273, 25541-25544).

- 5           CBP interacts with several general transcription factors. Swope et al. (*Id.*) demonstrated that TBP binds *in vitro* to the N-terminal end of CBP and Abrahams et al. (1993, *Oncogene* 8, 1639-1647) and Dallis et al. (1997, *J. Virol.* 71, 1726-1731) have shown that TBP binds CBP *in vivo*. TFIIB binds to the C-terminal end of CBP and this binding is blocked by the adenoviral protein E1A (Felzien et al., 1999, *Mol. Cell. Biol.* 19, 4261-4266).
- 10       Deletion of the TBP binding domain from CBP prevents it from acting as a co-activator for CREB whereas deletion of the TFIIB binding site has no effect (Swope et al., *Id.*). CBP also binds RNA helicase A and this association appears to be required for the interaction of CBP with RNA polymerase II (Nakajima et al., 1997, *Cell* 90, 1107-1112).

- Phosphorylation of CREB in the KID domain enhances its ability to activate
- 15       transcription and is mediated by a number of kinases (CAM kinase H and IV and protein kinase A) in response to biological stimuli such as neuronal signals or increased levels of intracellular cAMP (Gonzalez et al., 1991, *Mol. Cell. Biol.* 11, 1306-1312; Fiol et al., 1994, *J. Biol. Chem.* 269, 32187-32193; Sun et al., 1994, *Genes Develop* 8, 2527-2539). Specific phosphorylation of serine 133 within CREB promotes association with CBP but studies by
- 20       Sun and Maurer (1995, *J. Biol. Chem.* 270, 7041-7044) indicate this phosphorylation is not sufficient for activation of transcription. Other studies have found that phosphorylation of CREB on serines 129 and 142 modulate the ability of CREB to activate transcription (Fiolet et al., *supra*; Sun and Maurer, *supra*) suggesting they change the way in which CREB and CBP interact perhaps alters the function of CBP (e.g. the HAT activity or binding of other
- 25       proteins). The ability of CREB to activate transcription is also blocked by the MAPK inhibitor PD 98059 (Seternes et al., 1999, *Mol. Endocrinol.* 13, 1071-1083). Although the mechanism by which this occurs has not been completely elucidated other studies indicate that PD 98059 completely inhibits the ability of CBP to activate transcription (Liu et al., 1998, *J. Biol. Chem.* 273, 25541-25544).

- 30       Structure-function studies by Swope et al. (1996, *J. Biol. Chem.* 271, 28138-28145) indicated that deletion of amino acids 272-460 from the amino terminal end of CBP prevent it from acting as a co-activator for CREB. A CBP<sub>227-460</sub> peptide containing this deleted region als functions as a strong transcriptional activator when expressed as a Gal chimera (Gal-CBP<sub>227-460</sub>). In addition, overexpression of a CBP<sub>1-460</sub> peptide squelches the ability of full
- 35       length CBP to function as a CREB co-activator. Collectively, these studies suggest that a

factor binding to the amino terminal end of CBP is essential for it to function as a co-activator for CREB. These studies also indicate that CBP contains several regions which are involved in the activation of transcription and which function as transcriptional activators when expressed as gal-CBP chimeras (*Id.*). Various binding studies have identified a number of co-activators, general transcription factors, kinases, and transcription factors that contact these regions of CBP. A partial list is shown in Figure 1, where identification of the CBP domain that interacts with SRCAP is newly disclosed herein. See also Goldman et al., 1997, *Recent Progress in Hormone Research* 52, 103-1221.

A growing body of literature now illustrates the importance of CBP. The most compelling evidence for the importance of CBP has come from naturally occurring and artificially developed mutations. CBP appears to be critical in the development of the CNS, since a mutation in CBP has been associated with mental retardation in humans (Rubinstein-Taybi syndrome) (Petrij et al., 1995, *Nature* 376, 348-351). This hypothesis is strengthened by the finding that transgenic mice bearing similar CBP mutations have clinical features associated with Rubinstein-Taybi syndrome including: deficiency in long term memory, growth retardation, cardiac anomalies and skeletal abnormalities, and defects in hematopoiesis and vasculo-angiogenesis (Oike et al., 1999, *Blood* 93, 2771-2779; Oike et al., 1999, *Genetics* 8, 387-396). Mutations of CBP have also been found in a subset of patients with acute myeloid leukemia that have a t(8; 16)(p 11: p 13) chromosomal translocation which fuses CBP to the acetyltransferase MOZ (Burrow et al., 1996, *Nature Genetics* 383, 99-103).

The observation that mutations in CBP cause many distinct physiological defects is not surprising, since CBP serves as a co-activator for a wide variety of transcription factors. For example, CBP interacts with estrogen, progesterone, retinoic acid, vitamin D, glucocorticoid, and PPAR $\gamma$  receptors (reviewed in McKenna et al., 1999, *Endocrine Reviews* 20, 321-344), which are important for sexual maturation, bone development, lipid metabolism and regulation of energy metabolism. CBP interacts with transcription factors that direct pancreatic islet morphogenesis (NeuroD1/BETA2, Sharma et al., 1999, *Mol. Cell. Biol.* 19, 704-713) and liver development (HNF4, Dell et al., 1999, *J. Biol. Chem.* 274, 9013-9021). CBP also serves as a co-activator for a number of transcription factors activated by growth factors such CREB, jun, fos, smad proteins and NF-kappaB, as well as a number of constitutively active transcription factors such as c-myc, NF-1 C, GATA-1 and p53 (Dai et al., 1996, *Genes and Develop.* 10, 524-540; Chaudry et al., 1999, *J. Biol. Chem.* 274, 7072-7081; Hung et al., 1999, *Cell Biol* 19, 3496-3505; Lambert et al., 1998, *J. Biol. Chem.* 273, 33048-33053).

Competition or "cross talk" between transcription factors for the limiting amount of CBP present in the cell has been reported to be a control mechanism for cellular response to different signaling pathways. For example, competition between NF-kappaB and the tumor suppressor p53 for CBP determines whether p53 mediated apoptosis occurs (Webster et al., 1999, *Mol. Cell. Biol.* 19, 3485-3495). Competition between GR and NF-kappaB has also been reported as a control mechanism for glucocorticoid mediated repression of NF-kappaB-mediated inflammation (Sheppard et al., 1998, *J. Biol. Chem.* 273, 29291-29294). In LNCaP cells, overexpression of the androgen receptor can block AP-1 mediated transcription (Fronsdal et al., 1999, *J. Biol. Chem.* 273, 31583-31859).

CBP is critical for the functioning of several viruses that impact human health. This includes human T cell lymphotropic virus (HTLV-1), which recruits CBP to viral promoters through interaction of the viral protein TAX with CREB (Kwok et al., 1996). CBP also interacts directly with the viral transactivator protein Tat of human immunodeficiency virus type I (HIV-1) (Hottiger and Nabel, 1998, *J. Virol.* 72, 8252-8256). In humans, adenoviruses cause several diseases including: acute follicular conjunctivitis, pharyngoconjunctival fever, epidermic keratoconjunctivitis, acute hemorrhagic cystitis, cervicitis, infantile diarrhea, and respiratory tract infections in children. Immune compromised individuals such as those who have undergone bone or organ transplant or who have AIDS are particularly susceptible to adenoviral caused diseases (reviewed in Chapter 65 of Zinsser, 1992, *Microbiology*, 20<sup>th</sup> Ed., Joklik et al., Eds., Appleton and Lange). CBP interacts with several isoforms of the adenoviral protein E1A to mediate repression or activation of transcription (Felzien et al., 1999, *Mol. Cell. Biol.* 19, 42616). CBP also functions as a co-activator for the zta protein of Epstein-Barr virus (Zerby et al., 1999, *Mol. Cell. Biol.* 19, 1617-1626). Epstein-Barr virus infections have been associated with fatal lymphoproliferation in immune deficient patients and the development of Burkitt's lymphoma (reviewed in Zinsser *Microbiology*, 1992, *supra*). CBP has also been indirectly implicated in the transcriptional regulation of other viruses through interaction with CREB. For example, CREB binds to the enhancer of the IE1/2 gene of human cytomegalovirus (Lang et al., 1992, *Nucl. Acids Res.* 20, 3287-3295), an important pathogen in immunosuppressed patients such as transplant recipients and AIDS patients (Drew, 1988, *J. Infect. Dis.* 158, 449-456). CREB also binds the hepatitis B virus (HBV) enhancer element when complexed with the HBV protein, pX (Maguire et al., 1991, *Science* 252, 842-844).

A possible role of CBP in some forms of cancer is suggested by the observation that CBP is part of a multi-subunit complex with the breast cancer tumor suppressor BRCA1 and RNA polymerase II (Neish et al., 1998, *Nucl. Acids Res.* 26, 847-853). In some forms of

acute myeloid leukemia a t(7;11)(p15:p15) translocation results in the NUP98HOXA9 fusion protein, which is a strong transcriptional activator that uses CBP as a co-activator (Kasper et al., 1999).

CREB and, therefore, CBP have been implicated as possible effectors of a number of physiological responses in the central nervous system. In rats, acute morphine treatment increases the level of activated CREB in the locus coeruleus. This effect is attenuated with chronic treatment. Acute morphine withdrawal increases the level of activated CREB. Thus, regulation of genes by CREB may contribute to changes leading to addiction (Guitart et al, 1992, *J. Neurochem.* 58, 1168-1171). Furthermore, the level of phosphorylated CREB increases in the suprachiasmatic nuclei in response to light, suggesting it may be important for the entrainment of the pacemaker that controls hormonal and behavioral cycles (Ginty et al., 1993, *Science* 260, 238-241). In aplysia, the regimented application of serotonin to sensory neurons can be used to induce long-term memory. Analogs of cAMP are able to elicit some of the same responses suggesting CREB is involved. This hypothesis is supported by the finding that serotonin induces the phosphorylation of CREB (Kaang et al., 1993, *Neuron* 10, 427-435) and that microinjection of the oligonucleotides containing the binding site for CREB blocks serotonin induced long term memory (Dash et al., 1990, *Nature* 345, 718-721). Mice containing deletions in certain forms of CREB also appear to have defects in learning (Bourtchuladze et al., 1994, *Cell* 79, 59-68). Several lines of experiments also indicate CREB is involved in mediating the long-term effects of activity dependent plasticity at glutamatergic neurons (reviewed in Ghosh and Greenberg, 1995, *Science* 268, 239-247). A role of CBP is suggested by the recent studies by Hu et al. (1999, *Neuron* 22, 1-12), which indicate activation of glutamatergic neurons leads to an increase in the ability of CBP to activate transcription. This appears to be mediated by CaM kinases II and IV activated in response to increased calcium levels following depolarization and leads to phosphorylation of CBP (Hu et al., *Id.*).

Based on the importance of CBP in activating transcription, it would be desirable to identify other proteins that serve as transcriptional co-activators with CBP.

#### Summary of the Invention

Accordingly, the inventors have succeeded in discovering a protein, called SRCAP, for Snf2 Related CBP Activator Protein, that is a transcriptional co-activator for CREB binding protein (CBP). SRCAP is unlike all other known CBP co-activators in that it also is a Snf2 family member, and, as such, has ATPase activity. SRCAP also is capable of activating transcription without CBP and is also capable of interacting with DEAD box helicases, adenoviral DBP protein,  $\beta$ -actin and nuclear receptors. SRCAP is also capable of DNA

binding. Among the compositions also provided herein are fragments of SRCAP, polynucleotides encoding SRCAP or SRCAP fragments, complements of the SRCAP polynucleotides or fragments, and antibodies that specifically bind to SRCAP. These compositions are useful for, e.g., enhancing or suppressing CBP mediated transcriptional co-activation, and treatment of diseases involving inappropriate transcriptional activation that  
5 can be mediated by SRCAP or by CBP.

Thus, some embodiments of the present invention is directed to an isolated and purified SRCAP polypeptide. The polypeptide comprises the amino acid sequence of SEQ ID NO:2, or a conservatively substituted variant thereof, and wherein the polypeptide has  
10 ATPase activity and is capable of activating transcription. An example of a SRCAP polypeptide is provided as SEQ ID NO:2.

The present invention is also directed to an isolated and purified naturally occurring polypeptide comprising an amino acid sequence that has at least about 80% sequence homology to SEQ ID NO:2, wherein the polypeptide has ATPase activity and is capable of  
15 activating transcription. In preferred embodiments, the amino acid sequence that has at least about 90% sequence homology to SEQ ID NO:2.

In additional embodiments, the invention is directed to a polypeptide comprising at least 15 contiguous amino acids of any of the SRCAP polypeptides described above. In certain aspects, the polypeptide has at least one of the following SRCAP activities: ATPase,  
20 CREB binding protein (CBP) interaction and transcriptional co-activation, transcriptional activation without CBP, and DNA binding.

The present invention is also directed to a SRCAP chimera having a part of one of the above SRCAP polypeptides covalently attached to an amino acid sequence from a naturally occurring protein that is not a SRCAP. In preferred embodiments, the protein that is not  
25 SRCAP is a GAL4.

The present invention is further directed to a polynucleotide comprising a nucleic acid encoding any of the above-described SRCAP polypeptides. An example is SEQ ID NO:11. Complementary sequences to any of these polynucleotides are also provided, as are sequences that are capable of selectively hybridizing to the above sequences, as well as fragments of any  
30 of the polynucleotide sequences, where the fragment is at least 45 nucleotides long. These polynucleotides can be part of a vector used, e.g., to replicate the polynucleotide or express the encoded polypeptide. The vectors can also be used to create recombinant cells comprising any of the invention polynucleotides, and/or encoding any of the invention polypeptides. The cells can be, e.g., an *E. coli* cell or any other appropriate cell, including a mammalian  
35 cell. The cell can also be part of a living animal, including a mammal.

The above polynucleotides can also be capable of hybridizing to a SRCAP mRNA and, as such, can serve as an antisense agent. Ribozymes capable of specifically cleaving any of the invention polynucleotides is also provided, as are polynucleotides encoding any of the previously described chimeras.

5 In additional embodiments, the present invention is also directed to antibodies that specifically bind to any of the above described polypeptides. In a preferred embodiment, the antibody binds to amino acids 2733-2971 of SEQ ID NO:11.

Additionally, the present invention is directed to a method of activating transcription in a cell. The method comprises treating the cell with any appropriate polypeptide,  
10 polynucleotide, or antibody of the invention. In preferred embodiments, the cell is in a mammal, which includes humans. In some aspects, the method further comprises implanting the cell into a mammal after treating the cell.

The present invention is also directed to methods of detecting a SRCAP in a sample. The methods comprise treating the sample with one of the above-described antibodies, then  
15 determining whether the antibody specifically binds to a component of the sample. In these methods, specific binding indicates the presence of SRCAP in the sample. The sample can be from a mammal, including humans. In preferred embodiments, the determining step is by ELISA, RIA, or methods that include an electrophoresis step, such as western blot. For these methods, the sample can also be an intact tissue such as a tissue section.

20 In additional embodiments, the present invention is directed to a method of detecting any of the invention polynucleotides in a sample. The method comprises treating the sample with a second polynucleotide that specifically hybridizes with the polynucleotide of interest, then determining if the second polynucleotide specifically hybridized with a component of the sample. In some embodiments, the treating step is by a Southern hybridization method or a  
25 northern hybridization method.

The present invention is also directed to an additional method of detecting any of the invention polynucleotides in a sample. The method comprises treating the sample with a second polynucleotide that specifically hybridizes with the polynucleotide of interest, then performing a polymerase amplification method such as PCR or RT/PCR.

30 The present invention is further directed to methods of enhancing CREB binding protein (CBP)-mediated activation of transcription in a cell. The methods comprise treating the cell with one of the polypeptide, polynucleotide, or antibody compositions described above. As with previous methods, the cell can be part of a mammal, including a human.

The present invention is still further directed to a method for identifying a compound that modulates SRCAP protein function. The method comprises determining whether the candidate modulator compound alters the interaction of the SRCAP with CBP.

5 Additionally, the invention is directed to methods for identifying a compound that modulates SRCAP function. The methods comprise assessing the activity of SRCAP as an ATPase, in CBP interaction and transcriptional co-activation, in transcriptional activation without CBP, or in DNA binding in the presence of the candidate modulator compound.

In additional embodiments, the present invention is directed to a method for treating a patient having a disease involving a function affected by SRCAP protein. The method  
10 comprises administering an invention polypeptide or polynucleotide to the patient. In preferred embodiments, the patient is a mammal, including humans. Preferred functions are insufficient transcription of a gene selected from the group consisting of a gene mediated by CBP co-activation, a DEAD box RNA dependent helicase, an adenoviral DBP protein,  $\beta$ -actin and a nuclear receptor.

15 In further embodiments, the present invention is directed to a method for treating a patient having a disease mediated by SRCAP-activated transcription. The method comprises administering to the patient a compound that decreases SRCAP activity in the patient. Preferred compounds here are antibodies, antisense polynucleotides or ribozymes. In preferred embodiments, the disease is a virus infection, for example infection with  
20 adenovirus, HCV, HTLV-1, HIV-1, Epstein-Barr virus, cytomegalovirus or hepatitis B virus.

Brief Description of the Drawings

Figure 1 depicts domains within CBP that bind to other proteins. The discovery of the SRCAP binding domain is part of the present invention.

Figure 2A is a schematic of the SRCAP gene, where domains identified within  
25 the 2971 amino acid SRCAP are indicated including: two highly charged domains, the putative DNA binding domain, the CBP binding domain, and the position of the regions which make up the conserved ATPase domains (I, Ia-VI). The position of clone 11 identified by the yeast two hybrid screen as interacting with CBP and the position of the AB0002307 cDNA are also shown. Figure 2B shows a comparison of SRCAP  
30 conserved ATPase domains to other Snf2 related genes. The position of the amino acids at the C-terminal side of each conserved domain is indicated.

Figure 3 is a graph of measurements of the interaction of CBP with SRCAP in HeLa cells. The interaction of CBP and SRCAP cDNA (encoded by clone 11) was assessed using a mammalian two hybrid assay. HeLa cells were transfected with 300 ng  
35 of reporter gene pGAL-CAT and 600 ng of either pGal-CBP<sub>280-460</sub>, pGal-CBP<sub>227-410</sub>, or

pGal<sub>1-147</sub> and 600 ng of either pVP16, pVP16-clone 11, or pcDNA 3.1. The relative CAT enzymatic activity was determined by dividing CAT enzymatic activity of each sample by the transcriptional activity induced by the Gal-CBP<sub>280-460</sub> chimera. Values are the means and S.E. from three separate experiments in which each point was performed in triplicate.

Figure 4 is an autoradiograph demonstrating that anti-SRCAP antibodies immunoprecipitate a protein larger than CBP. Monoclonal antibodies raised against either the C-terminal end of SRCAP (amino acids 2733- 2971) or against E1A (M73 antibody, reference 18) were used to precipitate radiolabeled proteins from extracts made from 293 cells which were grown in the presence of <sup>35</sup>[S]-methionine/cysteine. Precipitated proteins were analyzed by SDS-PAGE and visualized using a PhosphorImager. The antibody against E1A has been previously shown to co-precipitate CBP/p300 with E1A. The position of CBP/p300 is indicated by the arrow on the right. The antibody against SRCAP precipitates a protein that migrates slower than CBP/p300. The position of the SRCAP protein is indicated by the arrow on the left.

Figure 5 is two graphs that demonstrate that SRCAP functions as an ATPase. The ability of SRCAP to function as an ATPase was assessed by measuring the ability of immunoprecipitated SRCAP to hydrolyze ATP. In figure 5A, increasing amounts of immunoprecipitated SRCAP (bound to protein sepharose A beads) or protein A beads (used in mock immunoprecipitation in the absence of antibody) were incubated with ATPase buffer containing 100  $\mu$ M cold ATP and 1  $\mu$ Ci <sup>32</sup>P- $\gamma$ -ATP and the amount of Pi released due to hydrolysis of ATP measured. Shown are three curves representing the total Pi released by the SRCAP-proteinA sepharose beads (upper), the non-specific Pi released by the mock immunoprecipitated protein A beads (lower) and the specific counts derived by subtracting the non-specific from the total Pi released (middle). In figure 5B, the K<sub>m</sub> for hydrolysis of ATP by SRCAP was measured by determining hydrolysis of ATP by 2  $\mu$ l of the SRCAP-protein A sepharose beads incubated with 1  $\mu$ Ci <sup>32</sup>P- $\gamma$ -ATP and either 10  $\mu$ M, 30  $\mu$ M, 100  $\mu$ M, or 300  $\mu$ M cold ATP. A plot of 1/[ATP] versus 1/d[Pi]/dT (1/ the change in Pi concentration over time) obtained at each concentration is shown. Values are the means and S.E. from three separate experiments and gives SRCAP a K<sub>m</sub> value for hydrolysis of ATP of 66  $\mu$ M.

Figure 6 is a graph of measurements of the activation of transcription by a Gal-SRCAP chimera. The ability of SRCAP to activate transcription was assessed by transient transfection assay. HeLa cells were transfected with 300 ng of the plasmid encoding the pGal-CAT reporter gene and equal molar amounts of either pGal CBP<sub>1-2441</sub>



(700 ng), pGal SRCAP<sub>1275-2971</sub> (592 ng plus 108 ng pcDNA 3.1), or pGal<sub>1-147</sub> (323 ng plus 377 ng pcDNA 3.1). The relative CAT enzymatic activity was determined by dividing CAT enzymatic activity of each sample by the transcriptional activity induced by the Gal-CBP<sub>1-2441</sub> chimera. Values are the means and S.E. from three separate experiments in which each point was performed in triplicate.

Figure 7 is a graph that demonstrates that SRCAP enhances transcription mediated by CBP. The ability of SRCAP to activate transcription of a Gal CBP chimera was assessed by transient transfection. HeLa cells were transiently transfected with 300 ng of the reporter gene pGal-CAT in the following combinations of plasmids: pGal CBP<sub>1-2441</sub> (700 ng plus 592 ng of pcDNA 3.1), pGal CBP<sub>1-2441</sub> (700 ng) and SRCAP<sub>1275-2971</sub> (592 ng), pGal SRCAP<sub>1275-2971</sub> (592 ng plus 592 ng pcDNA 3.1), pGal SRCAP<sub>1275-2971</sub> (592 ng), and pCBP<sub>1-2441</sub> (592 ng), pGal VP16 (50 ng plus 592 ng of pcDNA 3.1), or pGal VP16 (50 ng) and SRCAP<sub>1275-2971</sub> (592 ng). The relative CAT enzymatic activity was determined by dividing CAT enzymatic activity of each sample by the transcriptional activity induced by pGal CBP<sub>1-2441</sub> in the left panel, by the transcriptional activity induced by pGal SRCAP<sub>1275-2971</sub> in the middle panel, and by the transcriptional activity induced by pGal VP16 in the right panel. Values are the means and S.E. from three separate experiments in which each point was performed in triplicate.

Figure 8 is a graph that demonstrates that the adenoviral protein E1A disrupts interaction of CBP and SRCAP. The ability of E1A to disrupt CBP-SRCAP interaction was assessed by transient transfection. HeLa cells were transiently transfected with 300 ng of the reporter gene pGal-CAT, 600 ng of pGal CBP<sub>280-460</sub>, 600 ng of pVP16-clone 11 and either 50 or 200 ng of pE1A or pE1A RG2. Values are the means and S.E. from two separate experiments in which each point was performed in triplicate.

Figure 9 is a graph demonstrating the interaction of NS5A with SRCAP in a mammalian two hybrid system. HepG2 cells were transfected with 1 µg of G5E1b-CAT reporter gene, 2 µg of VP16-5A and 2 µg of Gal-SRCAP or Gal-ΔSRCAP. A CAT assay was performed 48 h post transfection. The amount of DNA was kept constant in each transfection by adding the empty vector DNA. SRCAP-NS5A hybrid shows high level of CAT activity as compared to Gal-SRCAP or NS5A alone.

Figure 10A depicts an autoradiograph, and figure 10B depicts immunoblots demonstrating that NS5A protein physically associates with SRCAP. In figure 10A, *in vitro* translated <sup>35</sup>S-methionine labeled CMV-SRCAP was subjected to pull-down analysis with His-NS5A or His-NMP-1 (negative control) fusion protein. Ten percent of the input protein (*in vitro* translated CMV-SRCAP) was loaded in the gel for comparison. The image was edited

from the same x-ray film. In figure 10B, *in vivo* coimmunoprecipitation of endogenous SRCAP with HCV NS5A is demonstrated. HepG2 cells were transfected with NS5A expression plasmid or empty vector plasmid. Cells were lysed after 48 h. Vector transfected (lane 1) and NS5A transfected (lane 2) cell lysates were immunoprecipitated with a monoclonal antibody to SRCAP. Immunoprecipitates were separated by SDS-7.5% PAGE and immunoblotted with a rabbit antibody to NS5A. A secondary antibody conjugate (anti-rabbit IgG/horseradish peroxidase, Amersham) was used for detection of the peroxidase signal by chemiluminescence (ECL). The molecular weight of the NS5A band was also ascertained from the migration of standard protein molecular weight markers. The same blot was reprobed with SRCAP specific antibody for detection of endogenous SRCAP (lanes 1 and 2).

Figure 11 illustrates the colocalization of transfected NS5A and endogenous SRCAP in HepG2 cells. Immunofluorescent staining was performed using a rabbit polyclonal antibody against NS5A (panel A) and a monoclonal antibody to SRCAP (panel B). Fluorescence images of panels A and B were superimposed digitally for fine comparison (panel C).

Figure 12 is a graph of measurements of the transcriptional regulation of p21 promoter by NS5A and SRCAP. Effector plasmid (CMV SRCAP and/or CMV-NS5A) was cotransfected with 4  $\mu$ g of WWP-luc as the reporter plasmid in HepG2 cells. The total amount of plasmid DNA (7  $\mu$ g) was kept constant by the addition of empty vector in each transfection. Cell extracts were prepared 48 h post-transfection and luciferase activity was determined. In each set of experiments, triplicate transfections were performed and relative luciferase activity is presented. p21 promoter activity was suppressed when NS5A and SRCAP was coexpressed.

Figure 13 depicts a RT-PCR analysis of the effect of NS5A and SRCAP on p21 mRNA levels. Panel A depicts a quantitative RT-PCR analysis for endogenous p21 or GAPDH mRNA from NIH3T3neo (lane 1) and NIH3T3NS5A (lane 2) cells. Panel B depicts the detection of luciferase mRNA by RT-PCR from transiently transfected p21-luciferase (lane 1), p21-luciferase with NS5A (lane 2), and p21-luciferase with NS5A and SRCAP (lane 3). GAPDH was used as an internal control.

Figure 14 is a graph demonstrating that SRCAP activates GR-mediated transcription. The ability of SRCAP to influence GR-mediated transcription of the MMTV promoter was tested by transient transfection. CHO cells were transiently transfected as indicated with 150 ng of the reporter gene MMTV CAT, 50 ng or 150 ng of GR, and 1200 ng of SRCAP. Eighteen hours post-transfection, dexamethasone was added to a concentration of  $10^{-6}$  M and 24 hours later the cells were harvested and CAT enzyme activity measured. Values are the means and S.E. from two separate experiments in which each point was performed in triplicate.

Figure 15 is a stained PAGE gel demonstrating that an anti-SRCAP monoclonal antibody immunoprecipitates SRCAP with several other proteins. Monoclonal antibodies raised against either the C-terminal end of SRCAP (amino acids 2733- 2971) or against p300/CBP were used to precipitate proteins from extracts of A549 cells. Immunoprecipitated proteins were analyzed by SDS-PAGE and visualized by silver staining.

Figure 16 is a schematic showing regions of SRCAP used to make Gal chimeras.

Figure 17 is a graph demonstrating that multiple regions within SRCAP function as Gal chimeras to activate transcription. The ability of Gal-SRCAP<sub>1-1186</sub>, Gal-SRCAP<sub>2316-2971</sub> and Gal<sub>1-147</sub> to activate transcription was compared to the activity of Gal-SRCAP<sub>1275-2971</sub>. HeLa cells were transiently transfected with the reporter gene pGal-CAT and equal molar amounts of each Gal chimera. Values are the means and S.E. from two separate experiments in which each point was performed in triplicate.

Figure 18 is a graph demonstrating that SRCAP activates transcription of the Vitellogenin 2 promoter. A549 cells were transfected with the reporter gene Vitellogenin 2 CAT and equal molar amounts of plasmids encoding SRCAP 1-2971, SRCAP 1275-2971, or SRCAP 1-1186. The relative CAT activity is reported compared to the transcriptional activity of the Vitellogenin 2 CAT reporter gene alone. Values are the means and S.E. from two separate experiments in which each point was performed in triplicate.

#### Description of the Preferred Embodiments

The procedures disclosed herein which involve the molecular manipulation of nucleic acids are known to those skilled in the art. *See generally* Fredrick M. Ausubel et al. (1995), "Short Protocols in Molecular Biology", John Wiley and Sons, and Joseph Sambrook et al. (1989), "Molecular Cloning, A Laboratory Manual", second ed., Cold Spring Harbor Laboratory Press, which are both incorporated by reference.

The present invention is directed to the identification and use of a newly discovered protein, SRCAP, or Snf2 Related CBP Activator Protein, which affects transcription. SRCAP interacts with CREB binding protein (CBP) amino acids 227-460 to enhance the ability of CBP to activate transcription. SRCAP is also able to activate transcription without CBP.

SRCAP is a Snf2 family member. The Snf2 family consists of a number of proteins with diverse functions including remodeling chromatin, regulation of transcription, and DNA repair (Reviewed in Cote, et al., 1994, *Science* 265, 53-60). Some Snf2 family members serve as part of chromatin remodeling complexes such as the yeast SWI/SNF assembly, which reorganize chromatin structure during transcription activation (Travers, 1999, *Cell* 96, 311-314). This reorganization facilitates the access of DNA binding proteins. In this context,

Snf2 family members are also called SWI2/SNF2. SWI2/SNF2 family members include *Drosophila* Brm, yeast Sth1, and human BRG1 and hBrm.

A common feature of the Snf2 family of proteins is the presence of a highly conserved domain called the Snf2 domain, which functions as an ATPase (Laurent et al., 1993, *Genes Dev.* 7, 583-591). This ATPase domain consists of seven highly conserved motifs interspersed with variable spacers of non-conserved sequences. As shown by the comparison of the ATPase motifs of various Snf2 family members in Figure 2B, the SRCAP ATPase domain is clearly a Snf2 domain.

Thus, in some embodiments, the present invention is directed to a SRCAP protein. SRCAP can be distinguished from any other known proteins by its ability to act as a CBP co-activator in combination with its ATPase activity. SRCAP is also capable of mediating transcription without CBP. SRCAP can be identified, e.g., by two-hybrid analysis of a cDNA library for encoded polypeptides that interact with CBP. See, e.g., Example 1, where a SRCAP is identified from a HeLa cell library using yeast and mammalian two-hybrid systems. An open reading frame (orf) derived from HeLa cell SRCAP cDNA encodes the 3118 amino acid SEQ ID NO:1; the 2971 amino acid SEQ ID NO:2 is the amino acid sequence encoded by the same cDNA, starting from the presumptive initiator ATG, which is the first ATG in the open reading frame that occurs in the context of the consensus Kozak sequence (Kozak, 1989, *J. Cell Biol.* 108, 229-241). As shown in Figure 2A, the conserved ATPase domain is created by combining seven discontinuous regions. These regions are termed Box I, covering the 12 amino acids 442-453 (GILADEMGLGKT; SEQ ID NO:3); Box 1A, covering the 12 amino acids 474-485 (LIIVPTSVMLNV; SEQ ID NO:4); Box II, covering the 14 amino acids 542-555 (WRYLILDEAQNIKN; SEQ ID NO:5); Box III, covering the 23 amino acids 572-594 (RLLLTGTPLQNSLMELWSLMHFL; SEQ ID NO:6); Box IV, covering the 12 amino acids 639-650 (FLLRRVKVDVEK; SEQ ID NO:7); Box V, covering the 29 amino acids 1855-1883 (FILSTRSGGVGLNLTGADTVVFYDSDWNP; SEQ ID NO:8); and Box VI, covering the 22 amino acids 1886-1883 (DAQAQDRCHRIGQTRDVHIYRL; SEQ ID NO:9) (Figure 2B). These conserved boxes combine to create an ATPase in SRCAP that is similar to the ATPase in other Snf2 family members. However, there are differences between the SRCAP ATPase and at least one other Snf2 family member ATPase. For example, the SRCAP ATPase activity is apparently not stimulated by DNA, as opposed to the ATPase activity of recombinant yeast Snf2, which is stimulated five-fold by DNA (Laurent et al., 1993, *Genes Dev.* 7, 583-591). However, it is believed that substitutions can be made in the SRCAP ATPase conserved sequences to replace any of the ATPase amino acids with amino acids in equivalent positions (as in Figure

2B) from any other Snf2 family member, while still retaining ATPase activity. Also, it is believed any or all of these conserved regions can be replaced in whole or in part with the equivalent regions of any other Snf2 family member, while still retaining ATPase activity. For example, the ATPase of yeast Snf2 can replace the SRCAP ATPase to create a SRCAP  
5 with an ATPase that is stimulated by DNA.

Other regions of SRCAP, as identified herein, are functionally important. The approximately first (N-terminal) 400 amino acids, as well as the amino acids about 1600-2500 are highly charged, being made up of clusters of acidic and basic residues (Figure 2A). These highly charged regions are important for activating transcription. Based on mammalian two-  
10 hybrid studies using hybrid clones encoding various fragments of the SRCAP cDNA, the first highly charged region is necessary for direct CREB activation, whereas the second highly charged region is necessary for CBP co-activation of transcription. In addition, the C-terminal domain of SRCAP contains four copies of the motif KR(R/K)RGRP(P/R) (Figure 2A), which is found in several DNA binding proteins, for example the chromosomal proteins  
15 D1 and HMG-1, where it apparently mediates the binding of these proteins to A-T rich regions by contacts in the minor groove of DNA (Ashley et al., 1989, *J. Biol. Chem.* 264, 8394-8401; Churchill et al., 1991, *TIBS* 16, 92-97). A similar motif is found in the C-terminal end of human homologs of yeast Snf2 (hSnf2 $\alpha$  and  $\beta$ ) and within the DNA binding domain of the Snf2 family protein CHD1 (Chiba et al., 1994, *Nucleic Acids Res.* 22, 1815-1820; Stokes  
20 et al., 1995, *Mol. Cell. Biol.* 15, 2745-2753). An additional area of SRCAP that is functionally important is a region within amino acids 1380-1699. This area interacts with CBP, allowing SRCAP to serve as a co-activator of CBP-mediated transcription. In addition, the areas within amino acids 1-1186 and 2316-2971 are at least two additional domains involved in activation of transcription without the help of CBP (see Example 3).

Reference to SRCAP herein should be construed to include Snf2 family members of  
25 any origin that are substantially homologous and biologically equivalent to human SRCAP characterized and described herein. Such proteins may be naturally occurring or have modifications that do not occur in any naturally occurring protein. Included are naturally occurring SRCAPs from any mammal or other vertebrates. A search of yeast and *Drosophila*  
30 genomic databases did not find sequences that were homologous to the SRCAP human cDNA sequence. Thus, it is believed that SRCAP is not present in insects or fungi. However, GenBank has sequences for bovine SRCAP (Accession No. AW660374) and mouse SRCAP (AZ079669). Therefore, SRCAP would be expected to be present in all mammals, and perhaps other vertebrates.

The term "substantially homologous" as used above means that the degree of sequence identity between SRCAP orthologs from human, mouse, or any other species, is greater than that between paralogs such as human SRCAP and human Snf2 or between any other two different Snf2 family members. To determine percent homology between two sequences, the two sequences are first aligned. A common method for aligning sequences is by the Clustal method (Higgins et al., 1992, *Cabios* 8, 189-191), as used for example in the Lasergene biocomputing software (DNASTAR, INC, Madison WI). Percent homology is then determined by calculating the number of identical amino acids in the aligned sequences is divided by the total number of amino acids in the reference sequence. Any sequence homologies discussed herein is determined after alignment by the Clustal method.

The term "biologically equivalent" as used above means that the SRCAP compositions of the present invention are capable of ATPase activity and co-activation of CBP, although they may not necessarily perform these functions to the same degree as the human SRCAP identified herein. While human SRCAP exemplified herein contains functions other than ATPase activity and co-activation of CBP (e.g., DNA binding, transcriptional activation without CBP), it is anticipated that some SRCAP variants, either naturally occurring or man made, could be deficient in these functions.

Based on the homology that exists between human SRCAP as identified herein and bovine and mouse SRCAPs given in GenBank as Accession Nos. AW660374 and AZ079669, respectively, as well as the homology between particular Snf2 family members of different species (Woodage et al., 1997, *Proc. Natl. Acad. Sci. USA* 94, 11472-11477), it is expected that the non-conserved regions of human SRCAP would have at least about 90% homology to the non-conserved sequences of SRCAP of other mammalian species, and at least about 80% homology among the non-conserved sequences of SRCAP from any species. However, the SRCAP proteins from other species can be identified not only by homology to other SRCAPs, but also by the ability of the protein to serve as a transcriptional co-activator with CRP along with its ATPase activity.

The present invention additionally includes the identification and use of the various portions of SRCAP having an identifiable function (i.e., ATPase, CBP interaction and transcriptional co-activation, transcriptional activation without CBP, and DNA binding). Thus, each of these functions, either with or without any of the other functions, can be utilized, e.g., in chimeras with other Snf2 family members to create novel Snf2 family members, or in two-hybrid interaction studies.

It is recognized that naturally occurring SRCAP can be modified, wherein certain substitutions can be made in the amino acid sequence while still substantially retaining

SRCAP biological activity. Thus, conservatively substituted SRCAPs, or portions thereof, which are biologically equivalent to naturally occurring SRCAPs or portions are also within the scope of the present invention. Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. Conservatively substituted amino acids can be grouped according to the chemical properties of their side chains. For example, one grouping of amino acids includes those amino acids have neutral and hydrophobic side chains (A, V, L, I, P, W, F, and M); another grouping is those amino acids having neutral and polar side chains (G, S, T, Y, C, N, and Q); another grouping is those amino acids having basic side chains (K, R, and H); another grouping is those amino acids having acidic side chains (D and E); another grouping is those amino acids having aliphatic side chains (G, A, V, L, and I); another grouping is those amino acids having aliphatic-hydroxyl side chains (S and T); another grouping is those amino acids having amine-containing side chains (N, Q, K, R, and H); another grouping is those amino acids having aromatic side chains (F, Y, and W); and another grouping is those amino acids having sulfur-containing side chains (C and M). Preferred conservative amino acid substitutions groups are: R-K; E-D, Y-F, L-M; V-I, and Q-H.

Certain non-conservative amino acid substitutions of SRCAP or SRCAP portions can also be identified as providing polypeptides with biological equivalence to naturally occurring SRCAP. For example, substitution of an amino acid residue in a SRCAP ATPase with a non-conservative amino acid at the same position in the ATPase of another Snf2 family member would be expected to provide a functional ATPase.

Naturally occurring SRCAPs can be discovered from any mammalian or other vertebrate species by known methods, for example by identifying polynucleotide sequences (genomic, mRNA, or cDNA) from that species that are capable of selective hybridization with a known SRCAP polynucleotide or fragment. By selective hybridization or specific hybridization it is meant that a polynucleotide preferentially hybridizes to a target polynucleotide. A polynucleotide that specifically hybridizes to a reference sequence can be of any length, for example, about 15 nucleotides up to about 100 nucleotides or up to about 1000 nucleotides or up to about 10,000 nucleotides or even greater. Specific hybridization to identify other mammalian or other vertebrate SRCAPs is preferably done under moderate or high stringency conditions which, as well understood by those skilled in the art, can readily be determined by adjusting several factors during hybridization and during the washing procedure, including temperature, ionic strength, length of hybridization or washing times, and concentration of formamide (see for example, Sambrook, Fritsch and Maniatis., *Molecular Cloning: a Laboratory Manual, 2d Ed., Vols. 1-3*, Cold Spring Harbor Laboratory

Press, Plainview N.Y., 1989). However, as is known, hybridization conditions may be adjusted without undue experimentation depending various factors including the length of the SRCAP probe, the region of the SRCAP gene where the probe was obtained, and the expected homology of the SRCAP gene being sought.

5 As previously discussed, any of the functional portions of SRCAP (e.g., ATPase, CBP interaction and transcriptional co-activation, transcriptional activation without CBP, and DNA binding) can be utilized with other polypeptides to form chimeras that confer the SRCAP function. Nonlimiting examples of such chimeras include: a SRCAP with a Snf2 ATPase to confer the ability of the Snf2 ATPase to be stimulated by DNA; an Snf2 with its ATPase replaced with a SRCAP ATPase to eliminate the ability of the Snf2 to be stimulated by DNA; and a chimera of a portion of SRCAP with the activation domain of the yeast transcriptional activator protein GAL4, for use in determining whether particular proteins interact with that portion of SRCAP in two-hybrid systems, as described in Chien et al., 1991, *Proc. Natl. Acad. Sci. USA* 88:9578-9582, and in Examples 1 -3 herein. Several particular SRCAP chimeras are also identified in the Examples. The latter chimera is especially useful for determining whether any particular polypeptide interacts with SRCAP. Nonlimiting examples of polypeptides that could be tested in this way are transcription factors, other co-activators, and hormones.

15 Fragments of SRCAP are also encompassed by the present invention. Such fragments may be of any length but preferably retain at least one of the biological functions of SRCAP or are antigenic. The minimum length of such biologically active or antigenic fragments can readily be determined by those skilled in the art using known techniques. Preferably, the minimum length of fragments of SRCAP is at least 8 amino acids, more preferably, at least 10 amino acids, still more preferably at least 12 amino acids, even still more preferably at least 15 amino acids and most preferably, at least 20 amino acids or greater.

20 Antigenic fragments of SRCAP are capable of eliciting SRCAP-specific antibodies when administered to a host animal. Included are smaller fragments that require conjugation to a carrier molecule to be immunogenic. Typically, antigenic fragments will be at least 5 or 6 amino acids in length and may be any length up to the full length of SRCAP. Preferably an antigenic fragment is 8, more preferably 10, still more preferably 12 amino acids in length, even still more preferably 15 amino acids in length and most preferably 20 amino acids or more in length. A preferred SRCAP fragment for producing anti-SRCAP antibodies is SRCAP amino acids 2733-2971 of SEQ ID NO:2, which is the C-terminal end of the translated GenBank cDNA sequence AB0002307, described in Example 1.



Methods for preparation of SRCAP or a fragment thereof include, but are not limited to chemical synthesis, recombinant DNA techniques or isolation from biological samples. SRCAP can be prepared by any of these methods without undue experimentation. Chemical synthesis of a peptide can be performed, for example, by the classical Merrifield method of solid phase peptide synthesis (Merrifield, *J Am Chem Soc* 85:2149, 1963) or the Fmoc strategy on a Rapid Automated Multiple Peptide Synthesis system (DuPont Company, Wilmington, DE) (Caprino and Han, *J Org Chem* 37:3404, 1972).

The present invention is also directed to polynucleotides encoding the above-described SRCAP, modified SRCAP, or SRCAP fragments, or chimeras comprising a portion of SRCAP. Included here are polynucleotides that are double stranded or single stranded, DNA or RNA, and coding strand or complementary strand. An example is SEQ ID NO:10, which is a cDNA open reading frame encoding human SRCAP, and which encodes SEQ ID NO:1. Another example is SEQ ID NO:11, which is the cDNA of SEQ ID NO:10 truncated to begin at the initiator ATG codon, and which encodes SEQ ID NO:2. However, due to the degeneracy of the genetic code, any particular SRCAP polypeptide or fragment, or any chimera comprising portions of SRCAP, can be encoded by numerous polynucleotide sequences, which can be readily identified by the skilled artisan. For various applications such as gene therapy or antisense treatment, any or all of the nucleotides of the polynucleotides can also be substituted with non-naturally occurring nucleotides to produce a nucleic acid mimic, as is known in the art (see, e.g., Nielsen, 2000, *Pharmacol. Toxicol* 86, 3-7).

Included in the polynucleotides of the invention are fragments of a SRCAP gene coding region or the complement, for example fragments of SEQ ID NO:10. These fragments can be used, e.g., as probes, primers (including PCR primers), antisense agents and for other purposes that would be known to the skilled artisan. They can be as short as 10 nucleotides long. More preferably, they are at least 20 nucleotides long, even more preferably at least 45 nucleotides long.

The present invention extends to the preparation of antisense nucleotides and ribozymes that may be tested for the ability to interfere with any particular SRCAP function. This approach utilizes antisense nucleic acid and ribozymes to block translation of a specific mRNA, either by masking that mRNA with an antisense nucleic acid or cleaving it with a ribozyme.

Antisense nucleic acids are DNA or RNA molecules that are complementary to at least a portion of a specific mRNA molecule. Reviews of antisense technology include: Baertschi, 1994, *Mol. Cell. Endocrinol* 101, R15-R24 (1994); Crooke et al., 1996, *Annu. Rev.*

*Pharmacol. Toxicol.* 36, 107-129 (1996); Alama et al., 1997, *Pharmacol. Res.* 36, 171-178.

In the cell, they hybridize to that mRNA, forming a double stranded DNA:RNA or

RNA:RNA molecule. The cell will not translate an mRNA in this double-stranded form.

Therefore, antisense nucleic acids interfere with the expression of mRNA into protein.

- 5 Oligomers of about fifteen nucleotides and molecules that hybridize to the AUG initiation codon are particularly efficient, since they are easy to synthesize and are likely to pose fewer problems than larger molecules when introducing them into organ cells. Antisense methods have been used to inhibit the expression of many genes *in vitro* [Marcus-Sekura, 1988, *supra*; Hambor et al. 1988, *J. Exp. Med.* 168, 1237). Preferably, synthetic antisense nucleotides
- 10 contain phosphoester analogs, such as phosphorothiolates, or thioesters, rather than natural phosphoester bonds. These unnatural phosphoester bond analogs are more resistant to degradation, increasing the stability, and therefore the efficacy, of the antisense nucleic acids.

In the genetic antisense approach, expression of the wild-type allele is suppressed because of expression of antisense RNA. This technique has been used to inhibit TK

- 15 synthesis in tissue culture and to produce phenotypes of the *Kruppel* mutation in *Drosophila*, and the *Shiverer* mutation in mice (Izant et al., 1984, *Cell* 36, 1007-1015; Green et al., 1986, *Annu. Rev. Biochem.* 55, 569-597; Katsuki et al., 1988, *Science* 241, 593-595). An important advantage of this approach is that only a small portion of the gene need be expressed for effective inhibition of expression of the entire cognate mRNA. The antisense transgene can
- 20 be placed under control of its own promoter or another promoter expressed in the correct cell type, and placed upstream of a polyA site such as the SV40 polyA site.

Ribozymes are RNA molecules possessing the ability to specifically cleave other single stranded RNA molecules in a manner somewhat analogous to DNA restriction endonucleases. Ribozymes were discovered from the observation that certain mRNAs have

25 the ability to excise their own introns. By modifying the nucleotide sequence of these RNAs, researchers have been able to engineer molecules that recognize specific nucleotide sequences in an RNA molecule and cleave it. Recent reviews include Shippy et al., 1999, *Mol. Biotechnol.* 12, 117-129 (1999); Schmidt, 1999, *Mol. Cells* 9, 459-463; Phylactou et al., *Meth. Enzymol.* 313, 485-506 (2000); Oketani et al., *J. Hepatol.* 31, 628-634 (1999). Because they

30 are sequence-specific, only mRNAs with particular sequences are inactivated.

Investigators have identified two types of ribozymes, *Tetrahymena*-type and "hammerhead"-type. *Tetrahymena*-type ribozymes recognize four-base sequences, while "hammerhead"-type recognize eleven- to eighteen-base sequences. The longer the recognition sequence, the more likely it is to occur exclusively in the target mRNA species.

- 35 Therefore, hammerhead-type ribozymes are preferable to *Tetrahymena*-type ribozymes for

inactivating a specific mRNA species, and eighteen base recognition sequences are preferable to shorter recognition sequences.

Another aspect of the invention relates to (e.g. expression) vectors suitable for the replication of the above polynucleotides, in particular a DNA or RNA polynucleotide, and including antisense and ribozymes. The vectors may be, for example, plasmid, virus or phage  
5 vectors provided with an origin of replication, optionally a promoter for the expression of the polynucleotide and optionally a regulator of the promoter. The vector may contain one or more selectable marker genes, for example an ampicillin resistance gene in the case of a bacterial plasmid or a neomycin resistance gene for a mammalian vector. The vector may be  
10 used in vitro, for example for the production of RNA, or used to transfect or transform a host cell. The vector may also be adapted to be used in vivo, for example in a method of gene therapy.

Preferably, the DNA in the vector is operably linked to a control sequence that is capable of providing for the expression of the coding sequence by a host cell. The term  
15 "operably linked" refers to a juxtaposition wherein the components described are in a relationship permitting them to function in their intended manner. A control sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under condition compatible with the control sequences. Such vectors may be transformed or transfected into a suitable host cell to provide for expression of a  
20 polypeptide of the invention.

Another aspect of the invention relates to recombinant cells transformed or transfected with the above-described vectors. This may be for the replication and expression of a polynucleotide according to the invention, including the sequence of SEQ ID NO:10 or 11, or a fragment thereof. The cells can be chosen to be compatible with the vector without  
25 undue experimentation, and may for example be bacterial, yeast, insect or mammalian. The cells can also be a part of a living animal, for example a vertebrate or mammal.

An additional aspect of the invention provides a process for preparing a SRCAP polypeptide which comprises cultivating a host cell transformed or transfected with an expression vector as described above under conditions providing for expression (by the  
30 vector) of a coding sequence encoding the polypeptide, and recovering the expressed polypeptide.

SRCAP or SRCAP fragments may be used as an immunogen to generate antibodies that recognize HCV. Such antibodies include but are not limited to polyclonal, monoclonal, chimeric, single chain, Fab fragments, and products of a Fab expression library. Various  
35 procedures known in the art may be used for the production of polyclonal antibodies to HCV.

For the production of antibodies, various host animals, including but not limited to rabbits, mice, rats, sheep, goats, etc., can be immunized, preferably by injection with the SRCAP or SRCAP fragment. Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (*bacille Calmette-Guerin*) and *Corynebacterium parvum*.

Polyclonal antibodies can be prepared by immunizing rabbits or other animals by injecting antigen followed by subsequent boosts at appropriate intervals. The animals are bled and sera assayed against purified SRCAP protein usually by ELISA or by bioassay based upon the ability to block the action of SRCAP. When using avian species, e.g. chicken, turkey and the like, the antibody can be isolated from the yolk of the egg.

For preparation of monoclonal antibodies directed toward SRCAP, any technique that provides for the production of antibody molecules by continuous cell lines in culture may be used. These include but are not limited to the hybridoma technique originally developed by Kohler and Milstein (1975, *Nature* 256, 495-497), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, 1983, *Immunology Today* 4, 72; Cote *et al.*, 1983, *Proc Natl. Acad. Sci. U.S.A.* 80, 2026-2030), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole *et al.*, 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). In an additional embodiment of the invention, monoclonal antibodies can be produced in germ-free animals (International Patent Publication No. WO 89/12690, published 28 December 1989). Also, chimeric antibodies (Morrison *et al.*, 1984, *J. Bacteriol.* 159, 870; Neuberger *et al.*, 1984, *Nature* 312, 604-608; Takeda *et al.*, 1985, *Nature* 314, 452-454) can be made, e.g., by splicing the genes from a mouse antibody molecule specific for SRCAP together with genes from a human antibody molecule of appropriate biological activity. Such human or humanized chimeric antibodies are preferred for use in therapy of human diseases or disorders (described *infra*), since the human or humanized antibodies are much less likely than xenogenic antibodies to induce an immune response, in particular an allergic response, themselves.

Single chain antibodies (U.S. Patent Nos. 5,476,786 and 5,132,405 to Huston; U.S. Patent 4,946,778) can also be produced that are SRCAP-specific. An additional embodiment of the invention utilizes the techniques described for the construction of Fab expression libraries (Huse *et al.*, 1989, *Science* 246, 1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

Antibody fragments that contain the idiotype of the antibody molecule can also be generated by known techniques. For example, such fragments include but are not limited to: the  $F(ab')_2$  fragment which can be produced by pepsin digestion of the antibody molecule; the  $Fab'$  fragments which can be generated by reducing the disulfide bridges of the  $F(ab')_2$  fragment, and the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent.

When short SRCAP fragments such as oligopeptides (defined herein as a polypeptide less than about 25 amino acids long) or short polypeptides are selected as candidates for the production of an antibody to SRCAP, it is preferred that the fragments are from hydrophilic regions of SRCAP, which are likely to be exposed in the mature protein. As is well known, when a small (e.g., <10,000 MW or about 75 amino acids) SRCAP fragment is used as an antigen, an immune response can be better elicited by immunizing with a conjugate of the fragment with an immunogenic carrier molecule such as bovine serum albumin or keyhole limpet hemocyanin.

Antibodies can be raised against SRCAP fragments that include one or more of the conserved regions (e.g., an ATPase box) such that the antibody can cross-react with other Snf2 family members. Alternatively, the antibodies can be raised against unique fragments of SRCAP in order to produce antibodies that do not cross-react with other proteins.

The polypeptide, polynucleotide and antibody compositions described above, including SRCAP, SRCAP fragments, modified SRCAP, chimeras comprising SRCAP portions, polynucleotides encoding and complementary to these polypeptides, antisense and ribozyme polynucleotides, vectors and host cells comprising the various polynucleotides, and antibodies reacting to the polypeptides, are variously useful for diagnostic and therapeutic purposes.

Due to the biological importance of SRCAP, it would be useful to be able to determine whether the SRCAP protein or mRNA is present in a sample. Preferably, the determination would be quantitative. Such methods are provided by the present invention.

SRCAP protein can be identified and/or quantified using an antibody. As previously discussed, the antibody is preferably prepared against a hydrophilic portion of SRCAP. The antibody is also preferably specific for SRCAP, such that no other protein in the sample of interest would be expected to cross-react with the antibody. However, antibodies directed against a region that is conserved between SRCAP and other proteins, such as the ATPase, would be useful in generating antibodies for identifying that group of proteins. For example, an antibody against the SRCAP ATPase would be expected to cross-react with other Snf2

family members, and would be useful for determining the presence of Snf2 family members in general.

Thus, the present invention provides immunoassay methods of detecting SRCAP in a sample. The method comprises treating the sample with an antibody that binds to the SRCAP, then determining whether the antibody specifically binds to a component in the sample, where specific binding indicates the presence of SRCAP. The sample can be derived from tissue or fluid, such as blood or urine. When it is desired to detect SRCAP in a tissue, the tissue is preferably first prepared, e.g., by grinding, etc., in order for substantially all of the SRCAP from the tissue to be available for antibody binding.

The method is not narrowly limited to any particular immunoassay, and may be readily adapted to, e.g., western blotting, immunodiffusion, immunoelectrophoresis, ELISA, radioimmunoassay (RIA), or fluorescence polarization immunoassay. See, e.g., *Basic and Clinical Immunology*, Sites and Terr, eds., Appleton & Lange, Norwalk, Conn. pp 217-262, 1991. These assays can also be utilized in protein microarrays to simultaneously analyze for many proteins including SRCAP (Leuking et al., 1999, *Anal Biochem* 270, 103-11). Qualitative and quantitative adaptations of any of these assays for use in detecting SRCAP can be devised without undue experimentation.

Several of the above methods can also be utilized to localize SRCAP in tissue sections, by methods well known in the art.

The present method also provides assays for determining the presence of SRCAP mRNA in a sample. To detect the presence of mRNA encoding SRCAP, a sample is obtained, e.g., from a patient or from cells in culture. The sample can be, e.g., from blood or from a tissue biopsy sample. The sample is preferably treated to extract the mRNA contained therein. The resulting mRNA from the sample may also be subjected to gel electrophoresis or other size separation techniques.

In some embodiments, the mRNA of the sample is contacted with a polynucleotide probe to form hybrid duplexes. The probe, which is complementary to a portion of the SRCAP mRNA, may be as short as ten nucleotides long. However, in preferred embodiments, the probe is at least 100 nucleotides long. The probes can be made by any method known in the art, for example by nick translation, random primer, or PCR methods. Preferably, the probe is labeled with any useful detectable label known in the art, including radioactive labels such as  $^{32}\text{P}$ , fluorescent labels such as 5'-tetramethylrhodamine, or fluorescein dyes, or hapten labels such as digoxigenin. The label allows detection of the duplex resulting from the hybridization of the labeled probe with SRCAP mRNA. In these hybridization methods, the mRNA is usually immobilized, e.g., on a membrane, before

treatment with the probe, such as in dot blot or northern blot methods, which are well known in the art. These assays can also be utilized in microarrays to simultaneously analyze for many mRNAs including SRCAP mRNA (Bowtell et al., 1999, *Nat Genet* 21, 25-32).

High stringency conditions can be used in order to prevent false positives, that is  
5 hybridization to non-SRCAP nucleotide sequences. When using sequences that are not perfectly complementary to an SRCAP-encoding polynucleotide or a fragment thereof, less stringent conditions could be used; however, this would be a less preferred approach because of the likelihood of false positives.

Alternatively, to detect mRNA encoding SRCAP, a polymerase amplification method  
10 such as polymerase chain reaction (PCR) or reverse transcriptase/polymerase chain reaction (RT/PCR) can be used. See, e.g., Example 2. The PCR and RT/PCR methods are well known in the art, and are preferred over the previously described hybridization methods when small samples are used or when greater sensitivity is desired.

A SRCAP target sequence in the reverse transcribed cDNA can be amplified and  
15 detected using any other known methodology such as ligase chain reaction methods, including gap LCR (G-LCR) and other variations, or self-sustained sequence replication (3SR) and its various modifications. In addition, the SRCAP mRNA can be detected directly by asymmetric gap LCR (AG-LCR). See, e.g., Leckie et al., "Infectious Disease Testing by Ligase Chain Reaction" in *Molecular Biology and Biotechnology*, R. A. Myers, ed., pp. 463-  
20 466, VCH Publishers, 1995.

As is well known, the above methods can be adapted, without undue experimentation, for the detection of various other polynucleotides of the present invention, for example SRCAP cDNAs or fragments of the SRCAP gene in genomic DNA. Such methods are useful, e.g., in various molecular biological methods such as cloning or subcloning efforts.

25 In other embodiments, the present invention is directed to methods for identifying a compound that modulates SRCAP protein function. The method comprises assessing the activity of SRCAP as a transcriptional activator, a modulator of CBP function, or an ATPase in the presence of the candidate modulator. Preferably, the SRCAP activity in the presence of the candidate modulator is compared with SRCAP activity in the absence of the modulator.  
30 The various activities of SRCAP can be determined by any method known in the art. Several of these methods are utilized in the Examples, for example, methods for determining SRCAP activity as a transcriptional activator; methods for determining modulation of CBP function; and methods for measuring ATPase activity.

The polypeptide, polynucleotide, and antibody compositions of the present invention  
35 can variously be administered to a mammalian or other vertebrate patient, including humans,

for therapeutic purposes. For these purposes, the compositions preferably also comprise a pharmaceutically acceptable carrier or diluent. Pharmaceutically acceptable carriers or diluents include those used in formulations suitable for oral, rectal, nasal, topical (including buccal and sublingual), vaginal or parenteral (including subcutaneous, intramuscular, intravenous, intradermal, intrathecal and epidural) administration. The carrier can also contain other pharmaceutically-acceptable excipients for modifying or maintaining the pH, osmolarity, viscosity, clarity, color, sterility, stability, rate of dissolution, or odor of the formulation. Similarly, the carrier may contain still other pharmaceutically-acceptable excipients for modifying or maintaining release or absorption or penetration across the blood-brain barrier. The formulations may conveniently be presented in unit dosage form and may be prepared by any of the methods well known in the art of pharmacy. Such methods include the step of bringing into association the active ingredient with the carrier that constitutes one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

The polypeptides, polynucleotides, and antibodies of the present invention can also be linked or conjugated with agents that provide desirable pharmaceutical or pharmacodynamic properties. For example, they can be coupled to any substance known in the art to promote penetration or transport across the blood-brain barrier such as an antibody to the transferrin receptor, and administered by intravenous injection. (See for example, Friden et al., *Science* 259:373-377, 1993). Furthermore, these compositions can be stably linked to a polymer such as polyethylene glycol to obtain desirable properties of solubility, stability, half-life and other pharmaceutically advantageous properties. (See for example Davis et al. *Enzyme Eng* 4:169-73, 1978; Burnham, *Am J Hosp Pharm* 51:210-218, 1994).

For nonparenteral administration, the compositions can also include absorption enhancers that increase the pore size of the mucosal membrane. Such absorption enhancers include sodium deoxycholate, sodium glycocholate, dimethyl- $\beta$ -cyclodextrin, lauroyl-1-lysophosphatidylcholine and other substances having structural similarities to the phospholipid domains of the mucosal membrane.

Such excipients are those substances usually and customarily employed to formulate dosages for parenteral administration in either unit dosage or multi-dose form or for direct infusion into the cerebrospinal fluid by continuous or periodic infusion.

The therapeutic or pharmaceutical compositions of the present invention can be administered by any suitable route known in the art including for example intravenous, subcutaneous, intramuscular, transdermal, intrathecal or intracerebral. Administration can be



either rapid as by injection or over a period of time as by slow infusion or administration of slow release formulation. For treating tissues in the central nervous system, administration can be by injection or infusion into the cerebrospinal fluid (CSF). When it is intended that the composition be administered to cells in the central nervous system, administration can be with one or more agents capable of promoting penetration of SRCAP across the blood-brain barrier.

Dose administration can be repeated depending upon the pharmacokinetic parameters of the dosage formulation and the route of administration used.

It is also contemplated that certain formulations containing SRCAP are to be administered orally. Such formulations are preferably encapsulated and formulated with suitable carriers in solid dosage forms. Some examples of suitable carriers, excipients, and diluents include lactose, dextrose, sucrose, sorbitol, mannitol, starches, gum acacia, calcium phosphate, alginates, calcium silicate, microcrystalline cellulose, polyvinylpyrrolidone, cellulose, gelatin, syrup, methyl cellulose, methyl- and propylhydroxybenzoates, talc, magnesium, stearate, water, mineral oil, and the like. The formulations can additionally include lubricating agents, wetting agents, emulsifying and suspending agents, preserving agents, sweetening agents or flavoring agents. The compositions may be formulated so as to provide rapid, sustained, or delayed release of the active ingredients after administration to the patient by employing procedures well known in the art. The formulations can also contain substances that diminish proteolytic degradation and promote absorption such as, for example, surface-active agents.

The specific dose is calculated according to the approximate body weight or body surface area of the patient or the volume of body space to be occupied. The dose will also be calculated dependent upon the particular route of administration selected. Further refinement of the calculations necessary to determine the appropriate dosage for treatment is routinely made by those of ordinary skill in the art. Such calculations can be made without undue experimentation by one skilled in the art based on the activity of SRCAP for a particular cell type *in vitro*. Exact dosages are determined in conjunction with standard dose-response studies. It will be understood that the amount of the composition actually administered will be determined by a practitioner, in the light of the relevant circumstances including the condition or conditions to be treated, the choice of composition to be administered, the age, weight, and response of the individual patient, the severity of the patient's symptoms, and the chosen route of administration.

In some embodiments of this invention, SRCAP may be therapeutically administered by implanting into patients vectors or cells capable of producing a biologically-active form of

SRCAP or a precursor of SRCAP, i.e. a molecule that can be readily converted to a biological-active form of SRCAP by the body. In one approach cells that secrete SRCAP may be encapsulated into semipermeable membranes for implantation into a patient. The cells can be cells that normally express SRCAP or a precursor of SRCAP or the cells can be transformed to express SRCAP or a precursor thereof. It is preferred that the cell be of human origin and that the SRCAP be human SRCAP when the patient is human. However, the formulations and methods herein can be used for veterinary as well as human applications and the term "patient" as used herein is intended to include human and veterinary patients.

Some embodiments of the invention are directed to methods of modulating transcription in a cell. The methods comprise treating the cell with an amount of a polypeptide, polynucleotide, or antibody composition of the invention sufficient to modulate transcription of the cell. The cell can be a cell in culture (in vitro) or within a living mammal or other vertebrate, including humans (in vivo). Ex vivo applications are also envisioned, where cells are removed from a mammal or other vertebrate, treated with the invention composition, then reimplanted in the vertebrate.

The method is useful for modulating transcription of any gene that is directly or indirectly affected by transcription factors or co-activators with which SRCAP interacts. Nonlimiting examples of such transcription factors or co-activators include CBP and the transcription factors and co-activators affected by CBP (see Example 1), DEAD box RNA dependent helicases (see Example 3), adenoviral DBP protein,  $\beta$ -actin, and glucocorticoid receptor (GR) and other nuclear receptors (see Example 3). However, the method encompasses any transcription factor or co-activator affected by SRCAP, whether now known or later discovered.

The co-activation of CBP by SRCAP is significant because of the large number of transcription factors for which CBP is a co-activator. As discussed in the Background of the Invention section and illustrated in Figure 1, CBP interacts with, for example, GR, P/CAF, p/CIP, CREB, STATs, TATA-binding protein (TBP), TFIIB, RNA helicase A, estrogen receptor, progesterone receptor, retinoic acid receptor, vitamin D receptor, glucocorticoid receptor, PPAR $\gamma$  receptor, jun, fos, smad, c-myc, NF- $\kappa$ B, GATA-1, and p53. Based on these interactions and other known effects of CBP, SRCAP interaction with CBP would be expected to affect a wide variety of systems, including central nervous system development, potentially alleviating the deleterious effects of Rubinstein-Taybis syndrome; acute myeloid leukemia; sexual maturation; bone development; lipid metabolism; regulation of energy metabolism; pancreatic islet morphogenesis; liver development; p53 mediated apoptosis; glucocorticoid mediated repression of NF- $\kappa$ B-mediated inflammation; various central

nervous system disorders such as addiction; hormonal and behavioral cycles; memory; and long-term effects of activity dependent plasticity at glutamatergic neurons. It would be expected that selective targeting of any of the above particular effects can be achieved by various methods, including the treatment of only specific organs or cell types. Such specific treatment can include the use of targeting methods such as those that utilize viral or microorganism tropism to particular organs or cell types, or targeted binding proteins, for example chimeras of SRCAP and monoclonal antibodies to target specific sites where the antibodies bind.

SRCAP would also be expected to affect several aspects of virus infection. Examples include the interaction of the HTLV-1 protein TAX with CREB; the interaction of CBP with the HIV-1 Tat protein; various effects of adenovirus infection due to the interaction of CBP with the adenovirus E1A protein; various effects of Epstein-Barr virus due to the interaction of CBP with the viral zta protein; various effects of cytomegalovirus due to the interaction of CREB with the enhancer of the viral IE1/2 gene; various effects of hepatitis B virus (HBV) due to the interaction of CREB with the viral protein pX; and various effects of hepatitis C virus due to the interaction of SRCAP with the viral protein NS5A (see Example 2).

The methods of modulating transcription in a cell described herein can be directed toward the reduction of transcription or the enhancement of transcription. Transcription can be enhanced in a target cell by treating the cell with various polypeptide compositions, including SRCAP and SRCAP fragments that, e.g., interact with CBP (fragments comprising SRCAP<sub>1380-1699</sub>) or activate transcription in the absence of CBP (fragments comprising SRCAP<sub>1-1186</sub> or SRCAP<sub>2316-2371</sub>). The SRCAP or SRCAP fragments can be administered to the cell by way of treatment with the polypeptides themselves, by therapeutic methods well known in the art; alternatively, the fragments can be administered through the translation of a polynucleotide that is administered as a gene therapy agent. The polynucleotides can be delivered through a DNA or RNA virus, or by direct treatment with a polynucleotide (Ilan et al., 1999, *Sem. Liver Disease* 19, 49-59; Widera et al., 2000, *J. Immunol.* 164, 4635-4640; Hewson, 2000, *Mol. Med. Today* 6, 28-35; Allen et al., 2000, *J. Immunol.* 164, 4968-4978; Mahato, 1999, *J. Drug Target* 7, 249-268).

Various treatments with the invention compositions can also reduce transcription affected by SRCAP, e.g., by reducing SRCAP levels in the cell. For example, transcription can be reduced in a target cell by treating the cell with an antisense SRCAP polynucleotide or a ribozyme, as is known in the art. Additionally, treatment of the cell with an anti-SRCAP antibody would be expected to reduce transcription. The above treatments to reduce SRCAP levels would be useful for, e.g., reducing the effects of the various viruses that depend on

CBP co-activation of viral transcription, and reducing the effects of hepatitis C virus on cell growth regulation (see Example 2).

The present invention also provides methods of treating a patient having a disease involving a function affected by SRCAP. The methods comprise treating a cell of the patient with an amount of a polypeptide, polynucleotide, or antibody composition of the invention sufficient to modulate transcription of the cell. As described *supra* in the context of the cell treatment methods, the treatment can be directed toward increasing the presence of SRCAP (e.g., by SRCAP or SRCAP fragment polypeptide or polynucleotide) or decreasing the presence of SRCAP (e.g., by antisense, ribozyme or antibody treatment). In particular embodiments, the function is insufficient transcription of a gene selected from the group consisting of a gene mediated by CBP co-activation, a DEAD box RNA dependent helicase (see Example 3), adenoviral DBP protein,  $\beta$ -actin, and a nuclear receptor. An example of a nuclear receptor is the glucocorticoid receptor (GR). In these embodiments, the cell is treated with a SRCAP polypeptide or SRCAP polynucleotide, or fragments thereof. In other embodiments, the function is undesired effects caused by HCV NS5A, HTLV-1 TAX protein, HIV-1 Tat protein, adenovirus E1A protein, Epstein-Barr virus zta protein, cytomegalovirus IE1/2 enhancer, hepatitis B virus (HBV) pX protein. As previously discussed, when reduction of transcription is desired, the cell may be treated with SRCAP antisense or ribozyme preparations, or with anti-SRCAP antibodies.

In additional embodiments, the present invention is directed to a method of treating a patient having a disease involving insufficient activity of a SRCAP protein. The method comprises administering a SRCAP protein or derivative or fragment thereof to the patient or administering a SRCAP polynucleotide or derivative or fragment thereof to the patient. In preferred aspects, the disease causes insufficient transcription of a gene selected from the group consisting of a gene mediated by CBP co-activation, a DEAD box RNA dependent helicase, adenoviral DBP protein,  $\beta$ -actin, and a nuclear receptor.

The present invention is also directed to compositions useful for studying the effects of SRCAP. These compositions comprise transgenic cells or non-human animals that express a recombinant SRCAP gene or fragment. The SRCAP gene or fragment could encode a SRCAP having substantially wild-type SRCAP activity, e.g., to study the effect of expression of increased amount of SRCAP. Alternatively, the SRCAP gene or fragment could encode a mutant nonfunctional SRCAP or a SRCAP fragment encoding only one or a few of the SRCAP activities (e.g., only the CBP co-activating portion), or could comprise an antisense or ribozyme inhibitor. The SRCAP gene or fragment could also be part of a chimera that has functions other than those of SRCAP.

Preferred embodiments of the invention are described in the following examples. Other embodiments within the scope of the claims herein will be apparent to one skilled in the art from consideration of the specification or practice of the invention as disclosed herein. It is intended that the specification, together with the examples, be considered exemplary only, with the scope and spirit of the invention being indicated by the claims which follow the examples.

#### Example 1

This example describes the identification and initial characterization of SRCAP.

##### Experimental procedures

10        *Plasmids* -To generate the plasmids pGal-CBP<sub>227-410</sub>, pGal-CBP<sub>280-460</sub> and pGal-CBP<sub>227-460</sub>, PCR was used to generate a cDNA fragment encoding CBP amino acids 227-460, 280-460, and 227-410 which contain a 5' *Xba*I and 3' *Bam*HI sites. These were subcloned into the plasmid pRSV Gal<sub>1-147</sub> (Swope et al., 1996, *J. Biol. Chem.* 271, 28138-28145) digested with *Xba*I and *Bam*HI. To generate the plasmid pVP16, PCR was used to

15        generate a cDNA fragment which encoded a Methionine followed by amino acids 412 to 491 of VP16 (Dalrymple et al., 1985, *Nucl. Acid. Res.* 13, 7865-7879) and which contained a 5' *Xba*I site and a 3' *Eco*RI site. This was subcloned into the plasmid pcDNA 3.1 (Invitrogen) digested with *Xba*I and *Eco*RI. The plasmid pVP16-clone 11 was generated by subcloning the clone 11 cDNA insert obtained by *Eco*RI and *Bam*HI

20        digestion of the pGAD clone 11, into *Eco*RI and *Bam*HI digested pVP16. The pAS1 CBP<sub>227-460</sub> plasmid was made using PCR to generate a cDNA fragment encoding amino acids 227-460 of CBP which contained *Eco*RI restriction sites at the ends. This was subcloned into the *Eco*RI site of the plasmid, pAS1. The plasmid pAS1 and the HeLa pGAD library were a gift of Paul MacDonald, St. Louis University, St. Louis MO. The

25        pGal-VP16 chimera was a gift of R. Maurer, Oregon Health Sciences University, Portland, OR. The pGal SRCAP<sub>1275-2971</sub> plasmid was generated by subcloning the cDNA insert encoding SRCAP amino acids 1275-2971 obtained by *Nhe*I and *Bam*HI digestion of the plasmid SRCAP<sub>1275-2971</sub> (described below) into pRSV Gal<sub>1-147</sub> digested with *Xba*I and *Bam*HI.

30        *Library Screen* -*S. cerevisiae* reporter host strain HF7c was co-transfected with the plasmid pAS1 CBP<sub>227-460</sub> and the pGAD-HeLa library using a yeast transfection kit (Clontech) and grown as described in Fields, S., 1993 (Methods: A companion to Meth. Enzymol. 5, 116-124) in the presence of 10 mM 3-amino-1,2,4-triazole. The plasmid corresponding to clone 11 was isolated and sequenced by the dideoxy sequencing method.

The cDNA corresponding to the AB0002307 sequence was generated by PCR. Briefly, complimentary PCR primers located at the beginning of the AB0002307 sequence and spaced about 1 kb apart were used to screen a human SKN plasmid library (Gift S. Amara, Vollum Institute, Portland, OR). These primers were designed to introduce restriction enzyme sites that allow assembly of the full length AB0002307 cDNA without introducing changes in the amino sequences. The 5'-most primer also encoded an initiator methionine and a consensus Kozak sequence. Following restriction digestion, the cDNA fragments were subcloned into the plasmid pcDNA 3.1 and named SRCAP<sub>1275-2971</sub>. The clone 11 cDNA was used to screen a cDNA plasmid library by homology. Using this approach a series of overlapping cDNAs were obtained that extended the SRCAP coding sequences to 9144 bp. The sequences of all the clones were confirmed on both strands using an ABI automated DNA sequencer and the composite sequence has been deposited in the GenBank (accession NM 006662).

*Transfections* - HeLa cells were maintained in Dulbecco's modified Eagle medium (DMEM) supplemented with 10% fetal bovine serum (FBS), 100 mg/ml penicillin and 100 mg/ml streptomycin and were seeded at  $1 \times 10^5$  cells per 3.5 cm dish 18 hours prior to transfection. Each transfection utilized 200-300 ng of the pGAL-CAT reporter (pGAL4/E1b TATA) plasmid (Swope et al., *supra*) and the indicated plasmids. The Lipofectamine transfection method was used according to the manufacturer's directions (Gibco BRL). Cells were harvested 48 hours after transfection and assayed for CAT activity using the phase-extraction method (Swope et al., *supra*). Results were normalized to protein levels as determined by Bradford assay.

*Immunoprecipitation* - For the labeling studies, A549 or 293 cells were incubated for one hour with methionine/cysteine-deficient DMEM, 10% FBS dialyzed against PBS (phosphate buffered saline), and penicillin/streptomycin, then metabolically labeled overnight in 1 ml deficient DMEM and 0.25 mCi  $^{35}$ [S]-methionine/cysteine (EXPRESS Label-NEN). Labeled cells were lysed in 1 ml p300 lysis buffer (Yaciuk et al., 1991, *Mol. Cell. Biol.* 11, 5389-5397) and the supernatant incubated with protein A sepharose beads and a monoclonal antibody raised to the C-terminal end of AB0002307 (SRCAP amino acids 2733- 2971). Immune complexes were washed extensively, then boiled two minutes in 20  $\mu$ l 2x Laemmli buffer and analyzed by SDS-PAGE. Radiolabeled proteins were visualized using a PhosphorImager. For the ATPase activity studies, nuclei of A459 cells were prepared by the method of Dignam et al. (1983, *Nucleic Acids Res.* 11, 1475-1489). The nuclei were incubated in p300 lysis buffer, centrifuged and SRCAP immunoprecipitated by addition of anti-AB0002307 monoclonal antibody and protein A beads to the supernatant. In parallel experiments,

control "mock" immunoprecipitations were performed by addition of protein A sepharose beads alone.

*ATPase assay*- Protein A beads containing the SRCAP protein were further washed with 1.0 M NaCl, 10 mM Na<sub>2</sub>PO<sub>4</sub>, pH 8, 0.5% Triton X100 to remove non-specifically bound proteins and followed by a final wash in ATPase buffer consisting of 20 mM Tris, pH 7.9, 0.1% Tween-20, 30 mM NaCl, 5 mM MgCl<sub>2</sub>, 0.5 mM DTT and 0.5 mg/ml BSA. The K<sub>m</sub> for ATP hydrolysis was determined as described by Cote et al. (20). Briefly, 2-3  $\mu$ l of SRCAP-protein A beads were incubated in 20  $\mu$ l of ATPase buffer containing various amounts of cold ATP (10-300  $\mu$ M) and 1  $\mu$ Ci <sup>32</sup>P- $\gamma$ -ATP (3000 Ci/mmole). Following a 20 minute incubation at 30° C the unhydrolyzed ATP was removed by the addition of 150  $\mu$ l of 10 mM phosphoric acid containing 5% activated charcoal (Sigma). The mixture was vortexed, centrifuged to pellet the charcoal and the supernatant removed to a new tube. An additional 150  $\mu$ l of the phosphoric acid/charcoal solution was added and the mixture vortexed, centrifuged and the <sup>32</sup>Pi in the supernatant counted. Specific <sup>32</sup>Pi released was determined by subtracting the non-specific counts obtained from the mock immunoprecipitated protein A beads. To ensure the ATPase assay was within the linear range, various amounts of SRCAP-protein A beads (1-6  $\mu$ l) were assayed as described in 100  $\mu$ M cold ATP and 1  $\mu$ Ci <sup>32</sup>P- $\gamma$ -ATP.

#### Results

A yeast two hybrid screen was employed to identify cDNA clones encoding proteins that contact CBP amino acids 227-460. In the initial screen an excess of fifty clones were obtained and these were further analyzed by DNA sequencing. This analysis indicated that clone 11 shared sequence identity with an uncharacterized cDNA reported in GenBank (AB0002307) (Figure 2A). A BLAST search with the AB0002307 sequences indicated it shared homology with two of the seven domains (V and VI) found within the ATPase domain conserved in proteins of the Snf2 gene family (Figure 2A). Because of this homology we decided to test whether the protein encoded by clone 11 interacted with CBP in mammalian cells. For this assay, we constructed a plasmid encoding a VP16-clone 11 chimera and co-transfected it with the plasmid encoding the Gal-CBP<sub>227-460</sub> chimera. In these studies, the VP16-clone 11 chimera consistently increased about 1.5-fold the ability of the Gal-CBP<sub>227-460</sub> chimera to activate transcription of the reporter gene pGal-CAT (data not shown). We reasoned that the small 1.5 fold activation of transcription observed occurred because the Gal-CBP<sub>227-460</sub> chimera is a very strong transcriptional activator. To circumvent this problem, we tested

the interaction of the VP16-clone 11 chimera with the Gal-CBP<sub>227-410</sub> and Gal-CBP<sub>280-460</sub> chimeras that contain small deletions that reduce but do not eliminate their ability to activate transcription. As shown in Figure 3, co-transfection of the plasmids encoding the VP16-clone 11 chimera with the plasmid encoding Gal-CBP<sub>280-460</sub> activates

5 transcription about 20-fold compared to that seen with the Gal-CBP<sub>280-460</sub> chimera alone. Co-transfection of the plasmid encoding Gal-CBP<sub>280-460</sub> with the plasmid encoding only the VP16 activation domain did not activate transcription, indicating that contact of the VP16-clone chimera with CBP is mediated by the clone 11 portion. The VP16-clone 11 chimera failed to activate transcription of the more active Gal-CBP<sub>227-410</sub> chimera or

10 Gal<sub>1-147</sub> indicating that transcriptional activation is not due to a non-specific effect.

Studies were also conducted to delineate the borders of the minimal SRCAP binding domain within CBP. For these studies, a mammalian cell assay was developed by determining whether a portion of SRCAP (amino acids 1380-1699), which was identified by the yeast hybrid screening to interact with CBP (see Example 1) also

15 contacted CBP in mammalian cells (Figure 3). In these studies, HeLa cells were co-transfected with a plasmid encoding a VP16-SRCAP<sub>1380-1699</sub> chimera and plasmids encoding either a Gal-CBP<sub>280-460</sub> chimera or a Gal-CBP<sub>227-410</sub> chimera along with a reporter gene (Gal-CAT) containing the binding site for Gal4. If interaction between the SRCAP moiety of the VP16-SRCAP<sub>1380-1699</sub> chimera occurred with the CBP portion of

20 either of these Gal-CBP chimeras, we would expect to see an increase in transcriptional activity. As shown in Figure 3, the VP16-SRCAP<sub>1380-1699</sub> chimera increased the transcription mediated by the Gal-CBP<sub>280-460</sub> chimera about 20-fold. In contrast, the VP16-SRCAP<sub>1380-1699</sub> chimera failed to activate transcription of the Gal-CBP<sub>227-410</sub> chimera indicating that the SRCAP binding domain of CBP resides within amino acids

25 280-460.

Based on the above results we decided to clone the remainder of the AB0002307 cDNA. Using a combination of approaches (PCR and plasmid library screening), a 9.1 kb cDNA was obtained (Figure 2A). This included the 5 kb of the AB0002307 cDNA and an additional 4.1 kb of new sequence at the 5' end of the molecule. Within the

30 AB0002307 sequence, we found several differences with the reported sequences including an additional 111 base pair insertion at nucleotide 4128. The 9.1 kb composite sequence contains a continuous open reading frame. It, however, does not contain a termination codon (in the coding frame) raising uncertainty as to whether the cDNA clones obtained encode the full length protein. The presumptive initiator ATG is

35 positioned at nucleotide 217 and is the first ATG in the open reading that occurs in the



context of a consensus Kozak sequence (Kozak, 1989, *J. Cell Biol.* 108, 229-241).

Using this ATG as a translational start site a protein of 2971 amino acids with a predicted molecular weight of 315 Kd is obtained. This size is consistent with immunoprecipitation studies in which anti-AB0002307 antibodies detect a protein that  
 5 migrates slower in SDS-PAGE gels than CBP (predicted molecular weight of 265 Kd) (Figure 4).

A search of the NCBI database with the AB0002307 sequence indicated that it contains a complete ATPase domain that consists of seven highly conserved regions (I, Ia-VI) which are dispersed over the length of the protein. Based on the homology to  
 10 Snf2 family members and, as described below, on the ability to enhance CBP-mediated transcription, we named this protein SRCAP (Snf2 Related CBP Activator Protein). A comparison of the amino acid sequence of the SRCAP ATPase domain to the amino acid sequence of the ATPase domains found in other members of the Snf2 family is shown in Figure 2B.

15 To test whether SRCAP, like other members of the Snf2 family, functions as an ATPase, we immunoprecipitated SRCAP protein from nuclear extracts of A549 cells using the anti-AB0002307 monoclonal antibody and protein A sepharose beads. Shown in Figure 5A incubation of the SRCAP-protein A beads in ATPase buffer containing 100  $\mu$ M cold ATP and 1  $\mu$ Ci  $^{32}$ P- $\gamma$ -ATP resulted in the release of  $^{32}$ Pi indicating the  
 20 hydrolysis of ATP was occurring. The specific ATPase activity due to SRCAP was determined by subtracting out the non-specific ATPase activity which bound to protein A in the absence of the anti-AB0002307 antibody. As shown, a linear increase in the specific ATPase activity was observed with increasing amounts of SRCAP-protein A beads. To determine the Km for the hydrolysis of ATP by SRCAP, 2  $\mu$ l of SRCAP-  
 25 protein A beads were incubated with 1  $\mu$ Ci  $^{32}$ P- $\gamma$ -ATP and either 10  $\mu$ M, 30 M, 100  $\mu$ M or 300  $\mu$ M cold ATP. A plot of  $1/d[\text{Pi}]/dT$  versus  $1/[\text{ATP}]$  for three experiment is shown in Fig. 4B and indicated SRCAP has a Km for hydrolysis of ATP of 66  $\mu$ M.

Several members of the Snf2 gene family have been found to regulate transcription when tethered to a promoter by a heterologous DNA binding domain. This  
 30 prompted us to ask whether SRCAP was a transcriptional activator. For these studies, we tested the ability of a plasmid encoding a Gal-SRCAP<sub>1275-2971</sub> chimera to activate transcription of the Gal-CAT reporter gene in HeLa cells. As shown in Figure 6, this chimera activated transcription about 12-fold over the level of transcription induced by Gal<sub>1-147</sub>, and to about the same level as that observed with the Gal-CBP<sub>1-2441</sub> chimera.

To test whether SRCAP influenced the ability of CBP to activate transcription, we co-transfected the plasmid encoding SRCAP amino acids 1275-2971 with the plasmid encoding Gal-CBP<sub>1-2441</sub>. As shown in Figure 7, SRCAP enhanced the ability of the Gal-CBP to activate transcription about 2.5 fold. This enhancement of transcription was specific since SRCAP did not enhance the ability of Gal-VP16 to activate transcription. Co-transfection of the plasmid encoding the CBP<sub>1-2441</sub> along with the plasmid encoding the Gal-SRCAP<sub>1275-2971</sub> chimera did not result in a further increase in transcription (data not shown). The inability of exogenously introduced CBP to activate SRCAP transcription activity suggests that CBP is either not limiting in HeLa cells or that SRCAP does not function to activate transcription by recruitment of CBP. Consistent with this latter hypothesis, we have found that a Gal-clone 11 chimera that encodes the CBP binding domain of SRCAP does not activate transcription in either HeLa or F-9 cells (data not shown).

Recent studies indicate that the adenoviral protein E1A binds to the amino terminal end of CBP and inhibits the ability of a Gal-CBP<sub>1-450</sub> chimera to activate transcription prompted us to determine whether E1A inhibits binding of SRCAP to CBP (Kurokawa et al., 1998, *Science* 279, 700-702). As shown in Figure 8, transfection of plasmids encoding wild type E1A decreased transcription stimulated by interaction of the Gal-CBP<sub>280-460</sub> with the VP16-clone 11 chimera. In contrast, co-transfection with a plasmid encoding an E1A mutant (RG2) which does not bind CBP did not disrupt SRCAP and CBP interaction.

#### Discussion

In this example, we disclose the cloning of SRCAP, a novel member of the Snf2 gene family. As previously discussed, the Snf2 domain, having ATPase activity, consists of seven highly conserved motifs interspersed with variable spacers of non-conserved sequences. The entire Snf2 domain is contained in about 400 amino acids in most Snf2 family members (Snf2, Iswi, Chd1, Rad16, and Mot-1) and is contained in about 670 amino acids in others (P113 and Hip 116) (Zhang et al., 1997, *Gene* 202, 31-37). The Snf2 domain of SRCAP is unique in that the ATPase domain is dispersed in a much larger region of about 1465 amino acids (Figure 2B). Despite the unique spacing between the conserved motifs, the conservation of residues within the ATPase domain is striking. Consistent with this homology we have found that SRCAP functions as an ATPase with a Km for ATP hydrolysis of 66  $\mu$ M which is similar to the reported Km for hydrolysis of ATP by yeast Snf2 of 45  $\mu$ M (Cote et al., 1994, *Science* 265, 53-60). The ATPase activity of recombinant yeast Snf2 protein (purified from bacteria) has been

reported to be stimulated five-fold by DNA (Laurent et al., 1993, *Genes Dev.* 7, 583-591). In contrast, the ATPase activity of SRCAP (purified from A549 cells) was not stimulated by DNA (data not shown). This result suggests that the regulation of the ATPase activity of SRCAP and yeast Snf2 may occur through distinct mechanisms.

- 5 However, we cannot rule out the possibility that the lack of DNA dependence observed for the ATPase activity of SRCAP is due to differences in the protein purification protocols used e.g. which may allow DNA to co-purify with SRCAP but not yeast Snf2.

The ATPase domain has been shown to be critical for the function of several Snf2 family members. The yeast Snf2 protein is the prototype of this family. It  
10 functions as part of a multiple subunit SWI/SNF complex that appears to alleviate the repression of transcription of some promoters induced by chromatin through a process termed chromatin remodeling (reviewed in Peterson et al., 1995, *TIBS* 20, 143-147). Although the specific mechanisms for chromatin remodeling are not completely known, it allows the binding of transcription factors to sites previously inaccessible due to the  
15 presence of nucleosomes. Mutant yeast Snf2 molecules in which the ATPase function has been deleted neither function in chromatin remodeling assays or are able to activate transcription (Laurent et al., *supra*). ATPase activity is also required for transcriptional repression mediated by the Snf2 family member MOT-1 (Auble et al., 1997, *Mol. Cell. Biol.* 17, 4842-4841) which utilizes ATP to dissociate TBP from DNA. However, as  
20 discussed below, the ATPase activity of SRCAP is not needed for SRCAP mediated transcriptional activation. While this result differs from that obtained for the yeast Snf2, an analogous finding has been reported for the human Snf2 protein (hSnf2 $\alpha$ ) (Muchardt et al., 1993, *EMBO J.* 12, 4279-4290). Similar to our studies with SRCAP, when human Snf2 $\alpha$  is tethered to DNA by a heterologous DNA binding domain, the ATPase function  
25 is not required for activation of transcription. However, the ATPase function is essential for hSnf2 $\alpha$  potentiation of glucocorticoid receptor mediated transcription (*Id.*). These findings suggest that activation of transcription by human Snf2 (and perhaps SRCAP) occurs through several distinct mechanisms, one requiring the ATPase function and one which does not.

- 30 It is believed that the highly charged C-terminal end of SRCAP contributes to the ability of SRCAP to activate transcription since, in the case of hSnf2 $\alpha$ , deletion of the analogous highly charged domain results in loss of transcriptional activity (*Id.*).

Examination of the primary structure of the SRCAP indicates that in addition to binding CBP, it also apparently binds to DNA. Shown in Figure 2A, the C-terminal  
35 domain contains four copies of the motif KR(R/K)RGRP(P/R) of which multiple copies

are also found in DNA binding proteins (chromosomal protein D1 and HMG-1), where it is thought to mediate the binding of these proteins to A-T rich regions by contacts in the minor groove of DNA (Ashley et al., 1989, *J. Biol. Chem.* 264, 8394-8401; Churchill et al., 1991, *TIBS* 16, 92-97). A similar motif is found in the C-terminal end of human

- 5 homologs of yeast Snf2 (hSnf2 $\alpha$  and  $\beta$ ) and within the DNA binding domain of the Snf2 gene family protein CHD1 (Chiba et al., 1994, *Nucleic Acids Res.* 22, 1815-1820; Stokes et al., 1995, *Mol. Cell. Biol.* 15, 2745-2753).

- The adenoviral protein E1A exerts several biological activities including transformation of cells and activation or repression of cellular and viral genes (reviewed in Moran, 1994, *Semin. Virol.* 5, 237-240). E1A blocks the ability of CBP to function as a co-activator for a number of transcription factors and binds to three distinct sites within CBP: Amino acids 1-460, amino acids 1805-1891, and amino acids 2058-2163 (Kurokawa et al., 1998, *Science* 279, 700-702; Yang et al., 1996, *Nature* 382, 319-324; Lundblad et al., 1995, *Nature* 374, 85-88; Arany et al., 1995, *Nature* 374, 81-85).
- 15 Understanding how association of E1A with CBP alters the ability of CBP to function as a co-activator has come from studies that demonstrate that E1A binding competitively excludes binding of several proteins shown to be critical for CBP co-activator function. Binding of E1A to CBP amino acids 1805-1891 prevents binding of the histone acetyltransferase P/CAF while E1A binding to CBP amino acids 2058-2163 prevents
- 20 binding of the co-activator P/CIP (Kurisawa et al, *supra*; Yang et al., *supra*). Although P/CAF also binds to amino acids 1-460 of CBP, competition between P/CAF and E1A binding has not been demonstrated. In our studies, we have found that E1A binding to amino acids 280-460 of CBP excludes the binding of SRCAP to CBP suggesting that this represents an additional method by which E1A represses the co-activator function of
- 25 CBP.

- The primary structure of SRCAP indicates that it belongs to the Snf2 family of proteins, which function to modify protein-DNA interactions suggesting that SRCAP plays a similar role. Consistent with this notion our results indicate that SRCAP interacts with CBP and influences its ability to activate transcription. Recent studies
- 30 have indicated that different promoters that utilize CBP to activate transcription have different requirements for co-activators. For example, both P/CAF and P/CIP have been found to be required for activation of a CRE-reporter gene while P/CIP but not P/CAF is required for transcription of a GAS-reporter gene (Korzue et al., 19989, *Science* 279, 703-706). It, therefore, seems likely that SRCAP may function to enhance CBP-
- 35 mediated transcription at some but not all promoters.

### Example 2

This example describes studies that reveal the interaction of SRCAP with the NS5A protein of hepatitis C virus (HCV). Hepatitis C virus (HCV) is an important cause of morbidity and mortality worldwide, causing a spectrum of liver disease ranging from an asymptomatic carrier state to end-stage liver disease (DiBisceglie, 1997, *Hepatology* 26,34S-38S; Purcell, R. H., 1994, *Proc. Natl. Acad. Sci. USA* 91, 2401-2406). The HCV genome encodes a single polyprotein precursor that is cleaved by both host and viral proteases to generate structural and non-structural proteins. The non-structural protein 5A (NS5A) is generated as a mature protein by the action of NS3 protease in conjunction with NS4A (Grakoui et al., 1993, *J Virol.* 67, 1385- 1395; Tanji et al., 1995, *J Virol.* 69, 3980-3986). NS5A is localized in the nuclear periplasmic membrane (Tanji et al., *supra*) and exists as phosphoproteins (p56 and p58), with the degree of phosphorylation accounting for the difference in size (Ide et al., 1997, *Gene* 201, 151-158; Kaneko et al., 1994, *Biochem. Biophys. Res. Commun.* 205,320-326; Reed et al., 1997, *J Virol.* 71,7187-7197). Phosphorylation status of NS5A differs amongst HCV genotypes (Hirota et al., 1999, *Virology* 257, 130-137). NS5A is phosphorylated by a cellular serine/threonine kinase, and Ser<sup>221</sup> represents a major phosphorylation site (Reed et al., 1999, *J. Biol. Chem.* 274, 28011-28018). However, this phosphorylation site is dispensable for interactions with NS4A and PKR. Sequence comparison of the regions surrounding the phosphorylation sites indicates an extremely high level of conservation between different strains of the HCV but the biological significance of phosphorylation is still undefined.

Recent studies suggest that HCV NS5A protein transcriptionally modulates cellular genes, promotes cell growth (Ghosh et al., 1999, *J. Gen. Virol.* 80, 1179-1183; Gale et al., 1999, *J. Virol.* 73, 6506-6516) and inhibits TNF- $\alpha$  mediated apoptotic cell death (A.K. Ghosh and R.B. Ray, unpublished observations). There is also evidence that two-thirds of the NS5A protein from the C-terminal fused with Gal4-DNA binding domain functions as a potent transcriptional activator (Tanimoto et al., 1997, *Biochem. Biophys. Res. Commun.* 236, 360-364; Kato et al., 1997, *J. Virol.* 71, 8856-8859). Viral proteins may influence cellular genes, which in turn may be involved in the regulation of oncogenes or tumor suppressor genes. Inactivation of these genes may be a mechanism for the disruption of normal cell growth. Host factors are important components for the modulation of virus replication. Viruses also produce proteins that may interact with host factors for viral persistence by disrupting normal cell cycle.

To further understand the functional role of HCV NS5A, the interaction of NS5A with cellular protein(s) by yeast two-hybrid screening was examined. Results from this study provided important information regarding the association of NS5A protein with SRCAP.

#### Experimental Procedures

5        *Yeast two-hybrid screening.* The entire cDNA coding region of HCV NS5A (genotype 1a, H strain) was fused in frame with the Gal4 DNA-binding domain into the pGBT9 plasmid vector (Clontech) at the EcoRI/SalI restriction sites (pGBT9-5A) and transformed into *Saccharomyces cerevisiae* yeast strain HF7c. The pGBT9-5A positive yeast colonies were grown in appropriate liquid medium lacking tryptophan and were subsequently transformed  
10        with library plasmids fused to the GAL4 activation domain, constructed in pGAD plasmid vector (Clontech) for screening of cellular partners. Colonies were selected on agar plates lacking histidine, tryptophan, and leucine over a 7-day period. Positive yeast transformants were picked up and replated for  $\beta$ -galactosidase assay by colony-lift filter procedure. A  
15        positive interaction was determined by the appearance of blue colonies. The  $\beta$ -gal positive colonies were grown on a selective medium for plasmid isolation. Isolated plasmids were transformed into *E. coli* KC8 strain and selected for the activation domain plasmids on M9-leu agar plates. The potential NS5A-interacting cDNA inserts were retransformed into the yeast strain HF7c bearing the pGBT9-5A fusion gene, and were grown on an appropriate  
20        selective medium for  $\beta$ -gal assay. Positive interacting cDNA clones were analyzed by nucleotide sequencing using an automated sequencer (ABI). Using Blast analysis, nucleotide and predicted amino acid sequences were compared with known protein sequences in GenBank.

*Mammalian two-hybrid analysis.* A mammalian expression plasmid encoding VP16, a hybrid polypeptide containing the transactivation domain of herpesvirus VP16 (Yu et al.,  
25        1998, *J. Biol. Chem.* 273, 25388-25592), was fused to NS5A (VP16-5A). Gal-SRCAP expression plasmid DNA (Johnston et al., *supra*) was used in this study. HepG2 and NIH3T3 cells were cotransfected with 1  $\mu$ g of Gal4 responsive reporter gene (G5E1b-CAT), 2  $\mu$ g of VP 16-5A, and Gal-SRCAP or Gal- $\Delta$ SRCAP effector plasmids. CAT assay was performed as described in Ghosh et al., *supra*. In all the transfection experiments, the  $\beta$ -galactosidase gene  
30        was included to normalize the transfection efficiency.

*In vitro pull-down experiment.* The NS5A genomic region was cloned in frame with histidine-tag (His-NS5A) into proExHTA plasmid vector (Life Technology, Inc), and expressed in *E. coli* BL21 cells. Bacterial extracts were immobilized onto Ni-beads and incubated with *in vitro* translated  $^{35}$ S-methionine labeled CNW-SRCAP. Beads were washed and proteins were  
35        analyzed by SDS-polyacrylamide gel electrophoresis, followed by autoradiography (Ghosh et al.,

1999, *Biochem. Biophys. Res. Commun.* 260, 405-409). His-MBP-1 (an unrelated protein) was used similarly as a negative control.

*Coimmunoprecipitation.* HepG2 cells grown in 35 mm plates were transfected with 1 µg of the CMV-NS5A or pcDNA3 control plasmid using lipofectamine (Life Technologies, Inc).

5 Cell lysates were prepared after 48 h of transfection in 0.3 ml of low stringency lysis buffer (150 mM NaCl, 10 mM Hepes, pH 7.6, 0.1 % Nonidet P-40, 5 mM EDTA) containing protease inhibitors (2 µg/ml aprotinin, 2 µg/ml leupeptin, 1 µg/ml pepstatin, and 1 mM phenylmethylsulfonylfluoride). Each of the cell lysates were incubated with monoclonal antibody to SRCAP and immobilized on staphylococcal ProteinA-Sepharose CL-4B beads  
10 (Pharmacia). Immunoprecipitates were separated by SDS-PAGE, followed by Western blot analysis using NS5A or SRCAP specific antibody.

*Immunofluorescence study.* HepG2 cells were grown on glass cover slips in DMEM-10% FBS. Cells grown overnight were transfected with CMV-NS5A using lipofectamine for immunofluorescence and colocalization studies using a method similar to that  
15 described in Taylor et al., 1999, *Science* 285, 107-110. Cells were washed after 48 h of transfection and fixed with 3.7% formaldehyde in PBS for 30 min. After fixing, cells were washed twice with PBS and permeabilized with 0.2% Triton X-100 in PBS for 5 min. Cells were incubated with a murine monoclonal antibody to SRCAP, anti-NS5A rabbit polyclonal antibody or both the antibodies for 1 h at room temperature. Cells were washed and incubated  
20 with fluorochrome-conjugated secondary antibodies for 30 min at room temperature. Finally, washed cells were mounted for confocal microscopy using Bio-Rad 1024 Confocal Microscope. Fluorescence images were superimposed digitally to allow fine comparison. Colocalization of green (FITC) and red (TRITC) signals in a single pixel produces yellow color while separated signals remain green or red.

25 *Quantitative RT-PCR.* Cytoplasmic RNA was isolated from NIH3T3 cells transfected with various plasmid DNAs, stable NIH3T3neo and NIH3T3NS5A cells (Gale et al., 1999, *J. Virol.* 73, 6506-6516) using PUREscript kit (Gentra System). RNA (2 µg) was used for reverse transcription-PCR (RT-PCR) as described previously (Ray et al., 1995, *Cancer Res.* 55, 3747-3751; Ghosh et al., 1999, *Gene* 235, 85-91). RT-PCR reaction was  
30 performed using specific primers for p21 cDNA (forward primer: 5' TGTCCGTCAGAACCCATGCG -3' [SEQ ID NO:12]; reverse primer: 5' AGGGCTTCCTCTTGGAGA3' [SEQ ID NO:13]), luciferase cDNA (forward primer: 5'TTCGCAGCCTACCGTAGTGT-3' [SEQ ID NO:14]; reverse primer: 5'CCCTGGAAGATGGAAGCGTT-3 [SEQ ID NO:15]) or glyceraldehyde 3-phosphate  
35 dehydrogenase (GAPDH) cDNA (forward primer: 5' AGAATCATCC

CTGCCTCTACTG-3' [SEQ ID NO:16]; reverse primer:

5'CATGTGGGCCATGAGGTCCACCAC- 3' [SEQ ID NO:17]). Reaction was carried out at 48°C for 45 min for reverse transcription, followed by PCR at 94°C for denaturing, 55°C for annealing, and 72°C for extension. For quantitative evaluation, we initially performed the RT-PCR reaction over a range of cycles (20, 25, 30, 35 and 40) and 25-30 cycles was observed to be within the logarithmic phase of amplification. GAPDH was used in the quantitative RT-PCR analysis as an internal control.

*Luciferase assay.* HepG2 cells were transfected with 4 µg of a reporter plasmid (WVP-luc, p21 promoter linked with luciferase gene), 2 µg of CMV-NS5A (suboptimal dose) and 1 µg of CMVSRCAP using lipofectamine. 48 h after transfection, luciferase activity was measured as previously described in Ghosh et al., 1999, *J. Gen. Virol.* 80, 1179-1183. Briefly, cells were treated with lysis buffer (Promega), and luciferase activity in the lysates was assayed by integrating the total light emission over 10 seconds using a luminometer (Optocomp II, MGM Instruments). The luciferase activity was normalized based on protein concentration.

## Results and Discussion

It was previously demonstrated that the NS5A protein of HCV transcriptionally modulates cellular genes and promotes murine fibroblast cell growth into a tumorigenic phenotype (Ghosh et al., 1999, *J. Gen. Virol.* 80, 1179-1183). Since the predicted amino acid sequence of NS5A does not possess a known DNA binding motif, it appears that NS5A transcriptionally regulates these cellular genes either by direct interaction with general transcriptional factor(s) or through a cofactor. To explore the potential targets of NS5A protein, a yeast two-hybrid screen was performed. Yeast strain HF7c was transformed with pGBT9-5A and colonies were selected on dropout agar medium lacking tryptophan. A few randomly picked colonies were grown and extracted proteins were subjected to SDS-PAGE followed by Western blot analysis using a monoclonal antibody to the Gal4 DNA binding domain. Results indicated pGBT9-5A fusion protein was expressed in all the yeast transformants (data not shown). The expression was also confirmed with a monoclonal antibody to NS5A. For the yeast two-hybrid screening, HF7c yeast cells expressing NS5A were transformed with library plasmid DNAs and selected the candidate colonies on the basis of their ability to grow in the appropriate selection medium and turning on the LacZ gene. Yeast transformants, positive for the activation of two reporter genes, were identified from  $2 \times 10^5$  independent transformants. We initially identified 30 β-gal positive clones grown in histidine deficient selective medium. Plasmid DNA was isolated from 17 clones, amplified in bacteria and retransformed into HF7c yeast cells expressing pGBT9-5A gene for confirmation of the positive interaction. Six clones indicated positive growth on selective medium and in the β-gal assay following retransformation. Upon further



testing of these clones for interaction with a battery of heterologous baits in yeast, three clones were found to specifically interact with pGBT9-5A and not with other heterologous protein baits. All three clones were sequenced and analyzed by the Blast program. Sequence analysis revealed that these isolates represent an independent overlapping cDNA with homology to a recently  
5 identified co-activator SRCAP (Johnston et al, *supra*).

The mammalian version of the conventional two-hybrid assay was used to ascertain whether the candidate NS5A-interacting protein associates with NS5A in mammalian cells. For this purpose, we constructed mammalian expression plasmid vectors that encode a VP16-5A and Gal-SRCAP fusion proteins. The mammalian two-hybrid assay was performed by transfecting  
10 HepG2 or NIH3T3 cells with a Gal4-responsive reporter gene (G5E1b-CAT) and pairwise combinations of the appropriate expression vectors. Reporter gene activity was determined by measuring CAT activity in cell lysates from each transfected culture. A significant increase in CAT activity was observed following co-expression of VP16-5A and Gal-SRCAP hybrids (Figure 9). However, CAT activity was not enhanced by co-expression of the VP16-5A and  
15 Gal4 vector. CAT activity was detected in Gal-SRCAP and VP-16 vector transfected cells, although the level of CAT expression was much lower as compared to hybrid. We obtained overlapping cDNAs of SRCAP interacting with NS5A from yeast two-hybrid assay. Initial mapping data suggests that NS5A associates with the C-terminal 62 amino acids of SRCAP. To confirm that the C-terminal region of SRCAP indeed interacts with NS5A, we used a C-terminal  
20 deletion mutant of SRCAP (Gal-ΔSRCAP) in the mammalian two-hybrid assay. Results demonstrated that the C-terminal deletion mutant can no longer interact with NS5A under a similar condition (Figure 9).

An *in vitro* binding assay was employed to verify the physical interaction between the viral protein NS5A and SRCAP. Histidine tagged NS5A (His-NS5A) was expressed in bacteria,  
25 immobilized onto Ni-beads and incubated with <sup>35</sup>S-methionine labeled SRCAP generated by *in vitro* translation. The proteins binding onto beads was then subjected to SDS-PAGE, followed by autoradiography. Results of the *in vitro* binding assay exhibited a specific band of SRCAP retained by the His-tagged NS5A-Ni beads (Figure 10A). However, an unrelated cellular protein (His-MBP-1), when used as a negative control under similar experimental conditions, failed to  
30 pull-down the SRCAP protein. Results from this *in vitro* experiment demonstrated that NS5A physically associates with SRCAP.

To investigate the ability of NS5A to associate with endogenous SRCAP *in vivo*, coimmunoprecipitation experiment was performed with lysates of NS5A transfected HepG2 cells. SRCAP specific antibody was used to precipitate the protein complex, followed by Western blot  
35 analysis with a specific antibody to detect the NS5A protein (Figure 10B). Interestingly, NS5A

was coprecipitated with endogenous SRCAP, as evident from the specificity of the antibody and the size of the NS5A protein in the immunoblot. Vector transfected control HepG2 cell lysates when analyzed similarly did not exhibit a NS5A specific band. The blot was stripped and reprobed with a specific antibody to SRCAP and an endogenous SRCAP band was detected in both the lanes. A similar experiment was performed using an unrelated monoclonal antibody of the same isotype as a negative control. This negative control antibody did not exhibit a detectable reactivity with either SRCAP or NS5A (data not shown). Results suggested that endogenous SRCAP form complex with HCV NS5A. Thus, specific association of SRCAP and NS5A in HepG2 cells was demonstrated using the mammalian two-hybrid system, *in vitro* pull-down assay and the coimmunoprecipitation analysis.

Further studies examined whether NS5A protein can colocalize with the endogenous SRCAP. We initially investigated the localization of endogenous SRCAP by indirect immunofluorescence in HepG2 cells using a monoclonal antibody to SRCAP. Immunofluorescent staining of the SRCAP protein showed a predominant perinuclear localization with occasional nuclear staining. Similarly, cells transfected with CMV-NS5A plasmid DNA, when stained with polyclonal antiserum, exhibits perinuclear staining (Tanji et al, 1995, *J. Virol.* 69, 3980-3986). To compare the subcellular localization of SRCAP with NS5A, HepG2 cells were transfected with CMV-NS5A and immunofluorescent staining was performed with antibodies to NS5A and SRCAP. Confocal microscopy showed a significant colocalization of the endogenous SRCAP with NS5A (Figure 11). There was no detectable staining when normal control sera were used. HCV may benefit by regulation of cellular gene(s) leading to the disruption of normal cell growth. Viral genes can override cellular control mechanisms which in untransformed cells regulates cell cycle progression in response to various antiproliferative signals. HCV often causes persistent infection and is a silent disease. In HCV persistently infected cells, the continued presence of viral gene products is likely to be detrimental for host cells, since HCV NS5A protein transcriptionally downregulates p21 activity (Ghosh et al., 1999, *J. Gen. Virol.* 80, 1179-1183). Cell cycle progression is driven by the sequential activation of cyclin-dependent kinases (CDKs) which are subject to regulation by positive (cyclins) and negative (CDK-inhibitory proteins) effectors (Morgan, 1995, *Nature* 374, 131-134). One such effector is the universal CDK inhibitor p21/waf 1 (Harper et al., 1993, *Cell* 75, 805-816; Yang et al., 1995, *Nature Med.* 1, 1052-1056). p21 may participate in apoptosis and increased p21 expression correlates with enhanced cell death under certain conditions (El-Deiry et al., 1993, *cell* 75, 817-825; Sheikh et al., 1995, *Oncogene* 11, 1899-1905). p21 protein binds and inhibits the activity of CDKs by preventing the phosphorylation of critical CDK substrates and by blocking cell cycle progression (Harper et al., 1993, *Cell* 75, 805-816; Xiong et al., *supra*). To

further examine the effects of NS5A and SRCAP on a natural promoter, HepG2 or NIH3T3 cells were transfected with a reporter construct (p21 promoter linked with luciferase gene), CMV-NS5A and CMV-SRCAP as the effector plasmids. Results from the luciferase assay suggested that inhibition of p21 promoter activity by NS5A protein was higher in presence of SRCAP (Figure 12). However, CMV-SRCAP alone at the same concentration did not show a significant effect on p21 promoter activity. A similar result was observed in NIH3T3 cells. To further examine the effect of NS5A on p21 promoter at the transcriptional level, a quantitative RT-PCR was performed using total RNA from stably or transiently transfected cells. This assay was designed to separately analyze the effect of NS5A and SRCAP directly on the p21 mRNA level or on the transcription of a tagged luciferase reporter gene. Results suggested downregulation of p21 promoter activity at the transcriptional level by NS5A alone or together with SRCAP (Figure 13).

This example discloses that SRCAP physically associates with HCV NS5A protein. SRCAP was isolated in three independently derived cDNA clones in yeast two-hybrid screening. The interaction of HCV NS5A protein with SRCAP was confirmed by mammalian two-hybrid assay, pull-down experiment and from coimmunoprecipitation studies. HCV NS5A colocalizes with SRCAP at the perinuclear membrane of HepG2 cells. Preliminary mapping analysis suggests that the binding of NS5A occurs with SRCAP through the C-terminus (62 amino acids), which contains highly charged residues. HCV NS5A also possesses several acidic domains (Tanimoto et al., *supra*; Kato et al., 1997, *J. Virol.* 71, 8856-8859). Whether the SRCAP binding domain of NS5A resides within one of these acidic domains remains to be elucidated. NS5A is suggested as a potent transcriptional activator. However, it exerts a negative regulatory activity on the p21 promoter in favor of promoting cell growth. SRCAP alone increases the E1b promoter activity when brought closer by Ga14 DNA binding domain to the promoter sequences (Johnston et al., *supra*). Although SRCAP is defined as a co-activator, it behaves like a corepressor when it associates with NS5A to exert a negative effect on the p21 promoter. We propose NS5A may recruit endogenous SRCAP to repress the p21 promoter. Transcription factors that activate in one circumstance and repress in another have been documented and the molecular basis for these transitions are quite diverse (reviewed in Roberts et al., 1995, *Nature* 375, 105-106; McKnight, 1996, *Genes Dev.* 10, 367-381). NS5A has recently been demonstrated to bind with the cellular factor Grb2 at the SH3 domain, which perturbs the mitogenic signaling pathways (Tan et al., 1999, *Proc. Natl. Acad. Sci. USA* 96, 5533-5538). Interaction between HCV NS5A and a SNARE-like protein (hVAP33) has also recently been reported (Tu et al., 1999, *Virology* 263, 30-41). Our observations add a novel cellular protein SRCAP to the list of NS5A interacting cellular factors. To our knowledge, this is the first report

dissecting the transregulatory activity of NS5A and implicating its relation with a cellular factor. We propose the recruitment of SRCAP by NS5A is one of the mechanisms for its transcription modulatory activity. This may also explain the growth promoting activity of HCV NS5A.

### Example 3

5           This example further characterizes SRCAP activities.

#### SRCAP regulates transcription of the MMTV promoter.

Examination of the primary sequence of SRCAP indicated it contains several LXXLL motifs, which have been found in other proteins to mediate interaction with nuclear receptors (McInerney et al., 1998, *Genes Devel.* 12, 3357-3368). This prompted us to test whether  
10       SRCAP might regulate glucocorticoid receptor (GR) mediated transcription. For these studies we tested the ability of SRCAP to regulate GR-mediated transcription of the MMTV promoter. As shown in Figure 14, we found that SRCAP enhanced GR-mediated transcriptional activation by 3 to 4-fold.

In experiments not shown, SRCAP in the absence of GR did not activate transcription  
15       of the MMTV promoter. This contrasts with our findings that SRCAP can directly activate transcription of the Vitellogenin A2 promoter.

#### SRCAP can be co-immunoprecipitated with several proteins.

To identify proteins that associate with SRCAP, we have developed a monoclonal antibody that recognizes the C-terminal end of SRCAP (amino acids 2733-2971). This was  
20       used to immunoprecipitate SRCAP from total cellular extract made by treating A549 cells with a low detergent lysis buffer that has been shown to maintain association of CBP with other cellular proteins (three-100 mm tissue dishes were used). Immunoprecipitated proteins were size fractionated on SDS-PAGE gels and proteins visualized by silver staining. Results are shown in Figure 15. The position of the 80 kD, 35, and 30 kD proteins which  
25       co-precipitated with SRCAP are shown by the arrows. The heavily stained proteins are the monoclonal antibody heavy and light chains.

To rule out the possibility that the co-precipitated proteins were contaminating serum proteins from the FBS in the cell culture media rather than bona fide A549 cellular proteins, we have repeated the immunoprecipitation using extracts made from cells metabolically  
30       labeled using <sup>35</sup>S-methionine. In these experiments, SRCAP, CBP, the 160-180 kD proteins, the 80 kD, 38 kD and the 30 kD proteins are <sup>35</sup>S-labeled indicating they are not serum proteins. We also wanted to rule out the possibility that these proteins are directly recognized by the anti-SRCAP monoclonal rather than being co-immunoprecipitated due to their association with SRCAP. To do this we have repeated the immunoprecipitation using cellular  
35       extracts made with lysis buffer having a high detergent content (RIPA buffer) which has been

shown to disrupt binding of p300/CBP with other cellular proteins (Wang et al., 1995, *J. Virol.* 69, 7917-7924). In the high detergent extract the anti-SRCAP antibody recognized only SRCAP but not CBP, the 160-180 kD proteins, or the 80 kD, 38 kD and 30 kD proteins (data not shown).

5 Collectively, the results of our immunoprecipitation studies indicate that proteins associated with SRCAP can be purified using the anti-SRCAP antiserum. To identify these proteins we scaled up our purification protocol. Extracts from twenty 150 mm plates were incubated with the anti-SRCAP antibody and immunoprecipitated proteins were size fractionated by SDS-PAGE gels and proteins visualized by staining with Coomassie brilliant  
10 blue. The bands corresponding to the 80 kD, 38 kD and 30 kD bands were excised and sent for MALD-MS analysis at the HHMI Biopolymer/W.M. Keck Foundation Biotechnology Resource Laboratory at Yale University. The result of this analysis indicated that the 80 kD protein is the X isoform of human DEAD box RNA dependent helicase. Interestingly, studies by others have indicated that DEAD box protein functions as a transcriptional activator  
15 regulated by association with a hepatitis C core protein (You et al., 1999, *J. Virology* 73, 2841-2853).

#### Characterization of the domains within SRCAP that activate transcription using Gal-SRCAP chimeras

20 As discussed in Example 1, the Gal-SRCAP<sub>1275-2971</sub> chimera activates transcription of a Gal-CAT reporter gene in HeLa cells.

To identify other regions within SRCAP that activate transcription, we generated and tested the transcriptional activity of two additional Gal-SRCAP chimeras. As shown in Figures 16 and 17, the Gal-SRCAP<sub>1-1186</sub> and Gal-SRCAP<sub>2316-2971</sub> chimeras also activate transcription. These results indicate SRCAP contains at least two domains involved in  
25 activation of transcription. One domain is located within SRCAP amino acids 1-1186 and the second domain is located within SRCAP amino acids 2316-2971. Since these regions of SRCAP activate transcription despite the lack of a CBP binding site, it indicates that SRCAP activates transcription at least in part through a CBP-independent mechanism.

We have also found that several SRCAP peptides (with no Gal<sub>1-147</sub> moiety attached)  
30 can activate transcription. As shown in Figure 18, SRCAP<sub>1-1186</sub>, SRCAP<sub>1275-2971</sub> and SRCAP<sub>1-2971</sub> proteins activated transcription of the *Xenopus* Vitellogenin A2 promoter. These same SRCAP peptides did not activate transcription of other reporter genes such as TK-CAT and SV-40-CAT. This result indicates that ability of the Gal-SRCAP<sub>1-1186</sub> and the Gal-SRCAP<sub>1275-2971</sub> to activate transcription due to presentation as a Gal chimera.

All references cited in this specification are hereby incorporated by reference. The discussion of the references herein is intended merely to summarize the assertions made by the authors and no admission is made that any reference constitutes prior art. Applicants reserve the right to challenge the accuracy and pertinence of the cited references.

5        In view of the above, it will be seen that the several advantages of the invention are achieved and other advantages attained.

As various changes could be made in the above methods and compositions without departing from the scope of the invention, it is intended that all matter contained in the above description and shown in the accompanying drawings shall be interpreted as illustrative and  
10    not in a limiting sense.

What is claimed is:

1. An isolated and purified SRCAP polypeptide, the polypeptide comprising the amino acid sequence of SEQ ID NO:2, or a conservatively substituted variant thereof, wherein the polypeptide has ATPase activity and is capable of activating transcription.
2. The polypeptide of claim 1, consisting essentially of SEQ ID NO:2.
3. An isolated and purified naturally occurring polypeptide comprising an amino acid sequence that has at least about 80% sequence homology to SEQ ID NO:2, wherein the polypeptide has ATPase activity and is capable of activating transcription.
4. The polypeptide of claim 3, comprising an amino acid sequence that has at least about 90% sequence homology to SEQ ID NO:2.
5. A polypeptide comprising at least 15 contiguous amino acids of the polypeptide of claim 3.
6. A polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:1.
7. The polypeptide of claim 6, wherein the polypeptide has a SRCAP activity selected from the group consisting of ATPase, CREB binding protein (CBP) interaction and transcriptional co-activation, transcriptional activation without CBP, and DNA binding.
8. A SRCAP chimera comprising the polypeptide of claim 5 covalently attached to an amino acid sequence from a naturally occurring protein that is not SRCAP.
9. The chimera of claim 8, wherein the protein that is not SRCAP is a GAL4.
10. A polynucleotide comprising a nucleic acid encoding the polypeptide of claim 1.
11. The polynucleotide of claim 10, comprising SEQ ID NO:11.
12. The polynucleotide of claim 10, consisting of SEQ ID NO:11.

13. A polynucleotide encoding the polypeptide of claim 3.

14. A polynucleotide encoding the polypeptide of claim 6.

15. A polynucleotide that comprises:

(a) SEQ ID NO:11;

(b) a sequence complementary to (a);

(c) a sequence capable of selectively hybridising to a sequence in either (a) or (b); or

(d) a fragment of any of sequences (a) to (c) that at least 45 nucleotides long.

16. A vector comprising the polynucleotide of claim 10.

17. A vector comprising the polynucleotide of claim 13.

18. A recombinant cell comprising the vector of claim 17.

19. The recombinant cell of claim 18, wherein the cell is an *E. colicell*.

20. The recombinant cell of claim 18, wherein the cell is a mammalian cell.

21. The recombinant cell of claim 20, wherein the cell is part of a living mammal.

22. The polynucleotide of claim 15, wherein the polynucleotide is capable of hybridizing to a SRCAP mRNA.

23. A ribozyme capable of specifically cleaving the polynucleotide of claim 13.

24. A polynucleotide encoding the chimera of claim 8.

25. An antibody that specifically binds to the SRCAP polypeptide or portion of claim

3.

26. The antibody of claim 25, wherein the antibody is a monoclonal antibody.



27. The antibody of claim 25, wherein the antibody binds to amino acids 2733-2971 of SEQ ID NO:11.
28. A method of activating transcription in a cell, comprising treating the cell with the SRCAP polypeptide of claim 1.
29. A method of activating transcription in a cell, comprising treating the cell with the SRCAP polypeptide of claim 3.
30. The method of claim 29, wherein the cell is in a mammal.
31. The method of claim 30, wherein the cell is in a human.
32. A method of activating transcription in a cell, comprising treating the cell with the SRCAP polynucleotide of claim 10.
33. The method of claim 32, further comprising implanting the cell in a mammal after treating the cell.
34. A method of activating transcription in a cell, comprising treating the cell with the SRCAP polynucleotide of claim 13.
35. The method of claim 34, wherein the cell is in a mammal.
36. A method of detecting a SRCAP in a sample, comprising treating the sample with the antibody of claim 25, then determining whether the antibody specifically binds to a component of the sample, wherein specific binding indicates the presence of SRCAP in the sample.
37. The method of claim 36, wherein the antibody binds to amino acids 2733-2971 of SEQ ID NO:11.
38. The method of claim 36, wherein the sample is from a mammal.
39. The method of claim 38, wherein the sample is from a human.

40. The method of claim 36, wherein the determining step is by ELISA or RIA.
41. The method of claim 36, wherein the determining step includes an electrophoresis step.
42. The method of claim 36, wherein the sample is an intact tissue.
43. A method of detecting the polynucleotide of claim 13 in a sample, comprising treating the sample with a second polynucleotide that specifically hybridizes with the polynucleotide of claim 13, then determining if the second polynucleotide specifically hybridized with a component of the sample.
44. The method of claim 43, wherein the treating step is by a Southern hybridization method or a northern hybridization method.
45. A method of detecting the polynucleotide of claim 13 in a sample, comprising treating the sample with a second polynucleotide that specifically hybridizes with the polynucleotide of claim 13, then perform a polymerase amplification method.
46. A method of enhancing CREB binding protein (CBP)-mediated activation of transcription in a cell, comprising treating the cell with the polypeptide of claim 1.
47. A method of enhancing CBP-mediated activation of transcription in a cell, comprising treating the cell with the polypeptide of claim 3.
48. The method of claim 47, wherein the cell is in a mammal.
49. A method of enhancing CREB binding protein (CBP)-mediated activation of transcription in a cell, comprising treating the cell with the polynucleotide of claim 10.
50. A method of enhancing CREB binding protein (CBP)-mediated activation of transcription in a cell, comprising treating the cell with the polynucleotide of claim 13.
51. A method for identifying a compound that modulates SRCAP protein function comprising determining whether a candidate modulator compound alters the interaction of the SRCAP protein of claim 4 with CBP.

52. A method for identifying a compound that modulates SRCAP function comprising assessing the activity of the SRCAP protein of claim 4 as an ATPase, in CBP interaction and transcriptional co-activation, in transcriptional activation without CBP, or in DNA binding.

5

53. A method for treating a patient having a disease involving a function affected by SRCAP protein comprising administering the polypeptide of claim 3 to the patient.

54. The method of claim 53, wherein the patient is a mammal.

55. The method of claim 54, wherein the patient is a human.

56. The method of claim 53, wherein the function is insufficient transcription of a gene selected from the group consisting of a gene mediated by CBP co-activation, a DEAD box RNA dependent helicase, adenoviral DBP protein,  $\beta$ -actin, and a nuclear receptor.

57. A method for treating a patient having a disease involving a function affected by SRCAP protein comprising administering the polynucleotide of claim 14 to the patient.

58. The method of claim 57, wherein the patient is a mammal.

59. The method of claim 58, wherein the patient is a human.

60. The method of claim 57, wherein the function is insufficient transcription of a gene selected from the group consisting of a gene mediated by CBP co-activation, a DEAD box RNA dependent helicase, adenoviral DBP protein,  $\beta$ -actin, and a nuclear receptor.

61. A method for treating a patient having a disease mediated by SRCAP-activated transcription comprising administering to the patient a compound that decreases SRCAP activity in the patient.

62. The method of claim 61, wherein the compound comprises an antibody.

63. The method of claim 61, wherein the compound comprises an antisense polynucleotide or a ribozyme.

64. The method of claim 61 wherein the disease is a virus infection.

65. The method of claim 64, wherein the virus is selected from the group consisting of adenovirus, HCV, HTLV-1, HIV-1, Epstein-Barr virus, cytomegalovirus and hepatitis B virus.

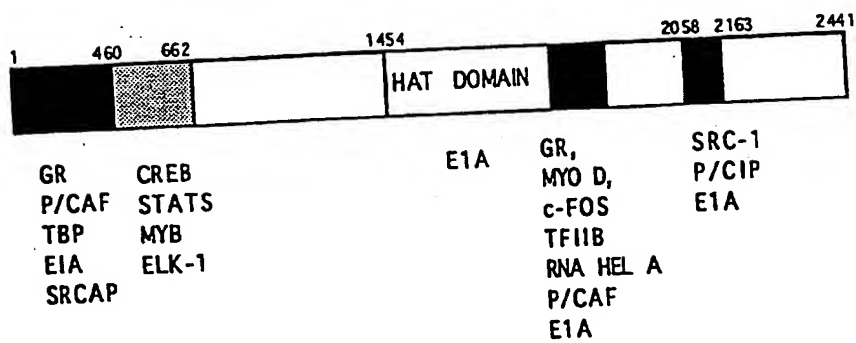


FIGURE 1

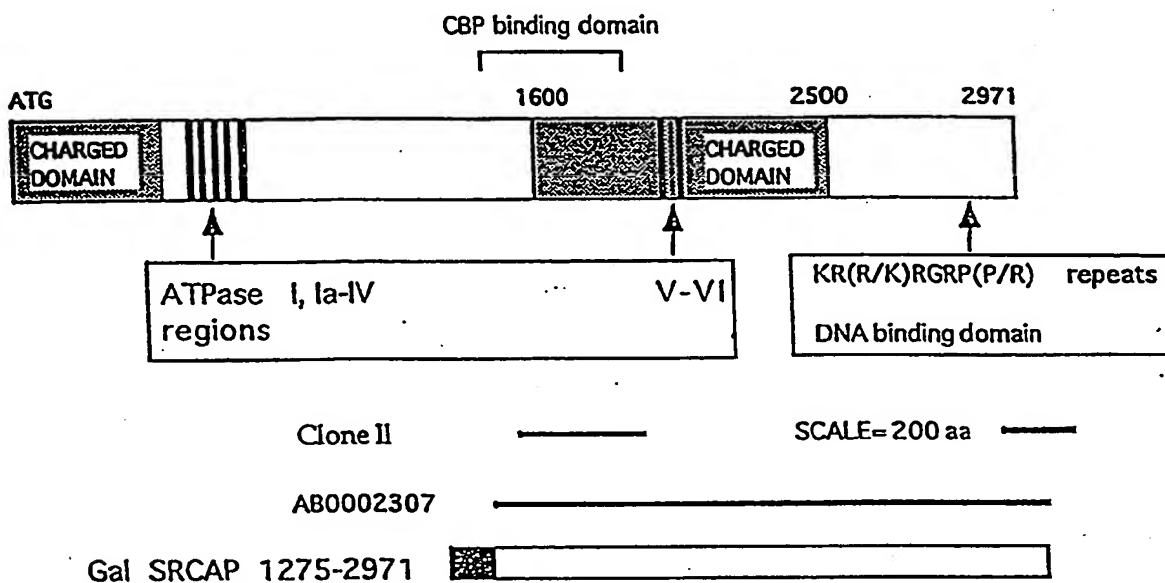


FIGURE 2A

	BOX I	BOX Ia	BOX II
SRCAP	GTTADENGLGKY 453	GLIVPTSVMLNT 485	GRVITIDEAQNIRN 555
P113	GTTADENGLGKY 301	GLICPTSVLSST 484	GLRVITIDEGHATRN 588
Hip116	GTTADENGLGKY 301	GLVICPTSVLSST 490	GLRVITIDEGHATRN 564
Snf2	GTTADENGLGKY 799	GLIVPTSVLSST 813	GLVHLITIDEGHATRN 901
Iswi	GTTADENGLGKY 160	IVIVKSTILO 192	GRVITIDEAQRIRN 263
Chd1	GTTADENGLGKY 511	GLVVPSTSTTS 543	GAFIGVDEPRIRN 619
Rad16	GTTADENGLGKY 217	GLVVAETVAQMO 245	FYRVITIDEAQRIRN 329
Mot1	GTTADENGLGKY 1304	GLICPTSLTGE 1347	YNYCVIDEGLIRN 1415
Hsnf2a	GTTADENGLGKY 752	GLIVPTSVLSST 784	GRVITIDEGHATRN 854
	BOX III	BOX IV	
SRCAP	RRLITGTPLONSLMELWSPMRL 594	SLRRVKVDYER 650	
P113	RVLITGTPLONSLKDLWSLISL 593	ILRRITKTSKIR 645	
Hip116	RVLITGTPLONSLKDLWSLISL 603	ILRRITKTSKIR 651	
Snf2	RRLITGTPLONSLMELWSPMRL 941	SLRRVKVDYER 1001	
Iswi	RRLITGTPLONSLMELWSPMRL 302	SLRRVKVDYER 350	
Chd1	RRLITGTPLONSLKDLWSLISL 658	SLRRVKVDYER 702	
Rad16	RRLITGTPLONSLKDLWSLISL 368	ILRRITKTSKIR 452	
Mot1	RRLITGTPLONSLMELWSPMRL 1454	SLRRVKVDYER 1514	
Hsnf2a	RRLITGTPLONSLMELWSPMRL 894	SLRRVKVDYER 952	
	BOX V	BOX VI	
SRCAP	SLSTRAGGGLGGLATADTVIIPDADNEHODLQAODRCHRIQOTRDVIRI 1907		
P113	SLSTRAGGGLGGLATADTVIIPDADNEHODLQAODRCHRIQOTRDVIRI 953		
Hip116	SLSTRAGGGLGGLATADTVIIPDADNEHODLQAODRCHRIQOTRDVIRI 960		
Snf2	SLSTRAGGGLGGLATADTVIIPDADNEHODLQAODRCHRIQOTRDVIRI 1211		
Iswi	SLSTRAGGGLGGLATADTVIIPDADNEHODLQAODRCHRIQOTRDVIRI 555		
Chd1	SLSTRAGGGLGGLATADTVIIPDADNEHODLQAODRCHRIQOTRDVIRI 910		
Rad16	SLSTRAGGGLGGLATADTVIIPDADNEHODLQAODRCHRIQOTRDVIRI 744		
Mot1	SLSTRAGGGLGGLATADTVIIPDADNEHODLQAODRCHRIQOTRDVIRI 1756		
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FIGURE 2B

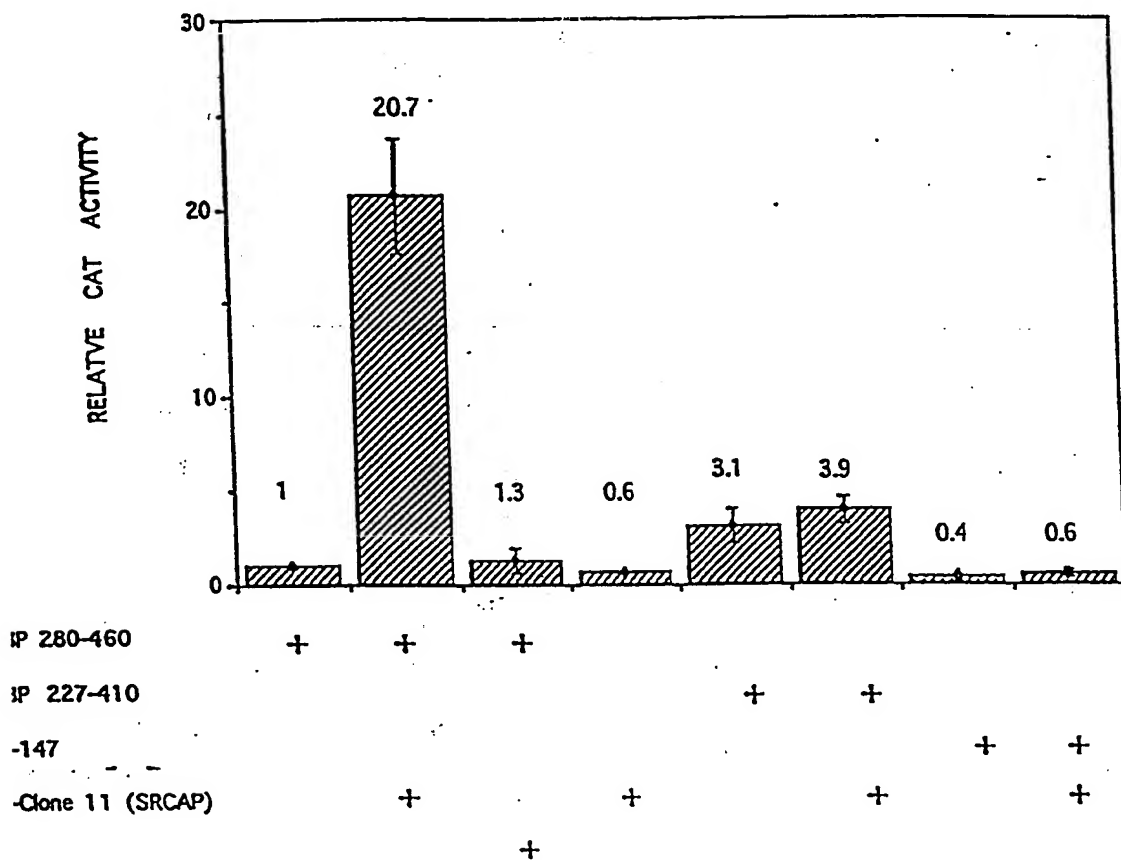


FIGURE 3



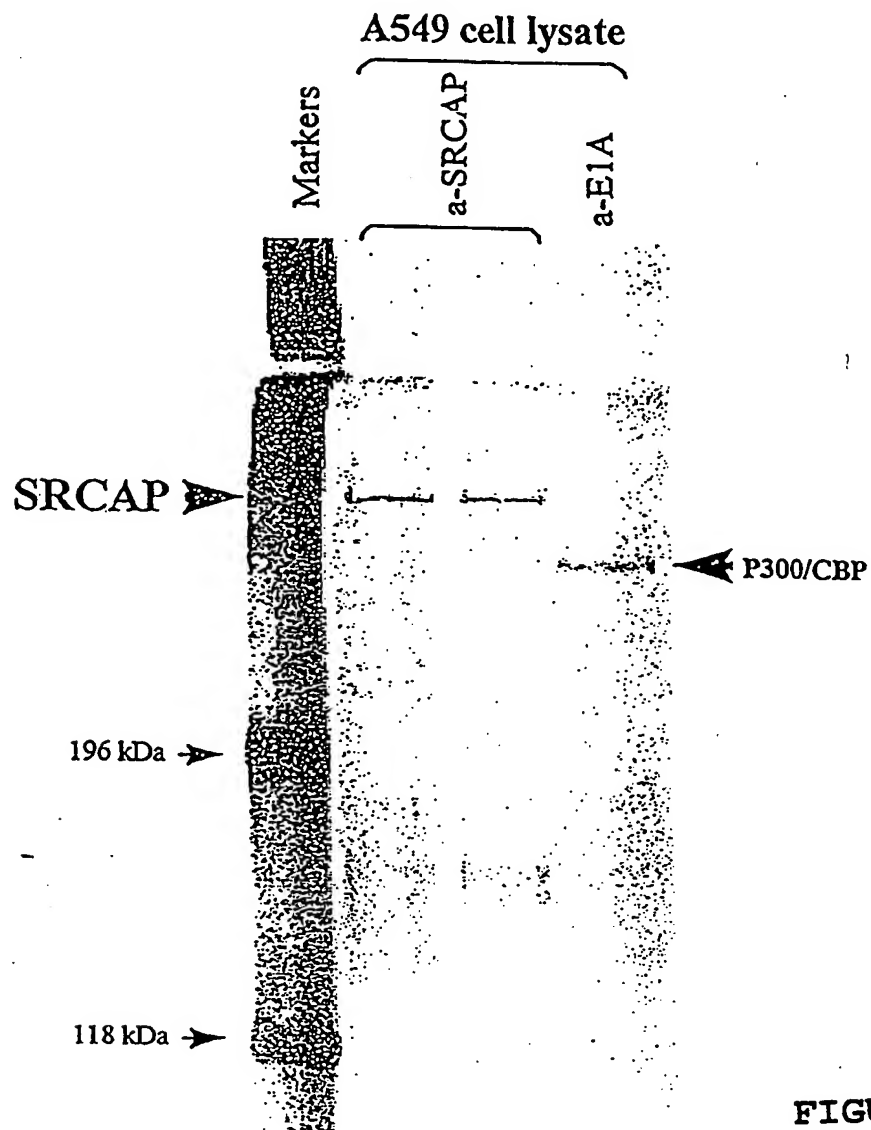


FIGURE 4

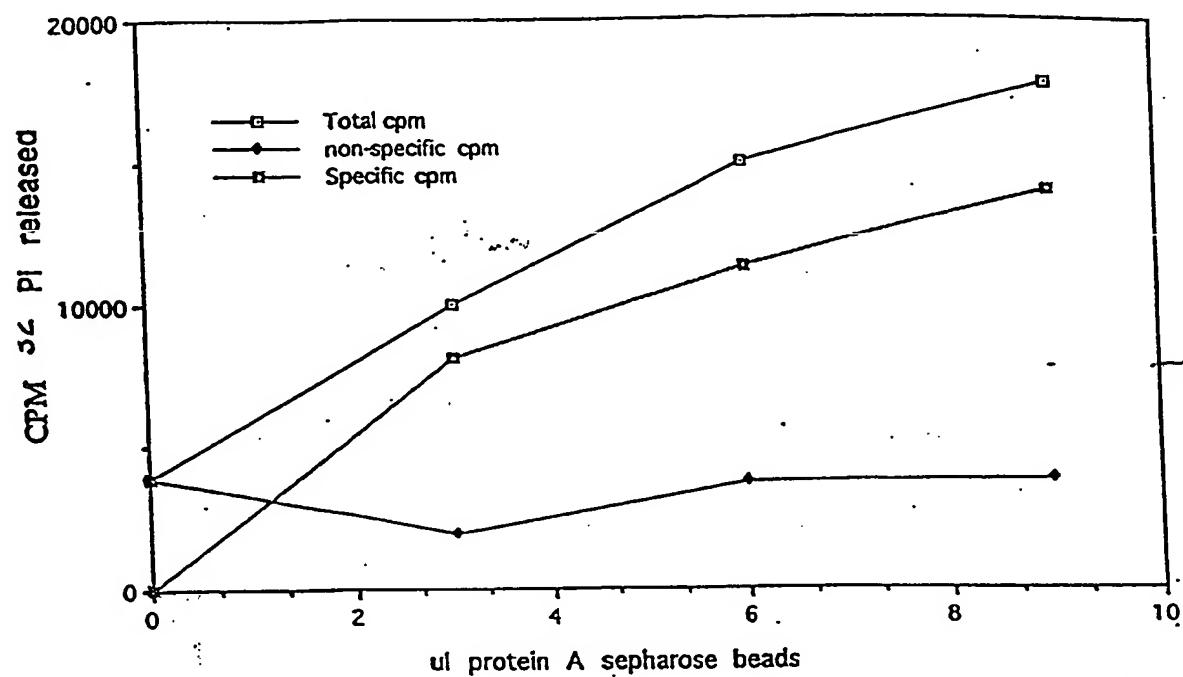


FIGURE 5A

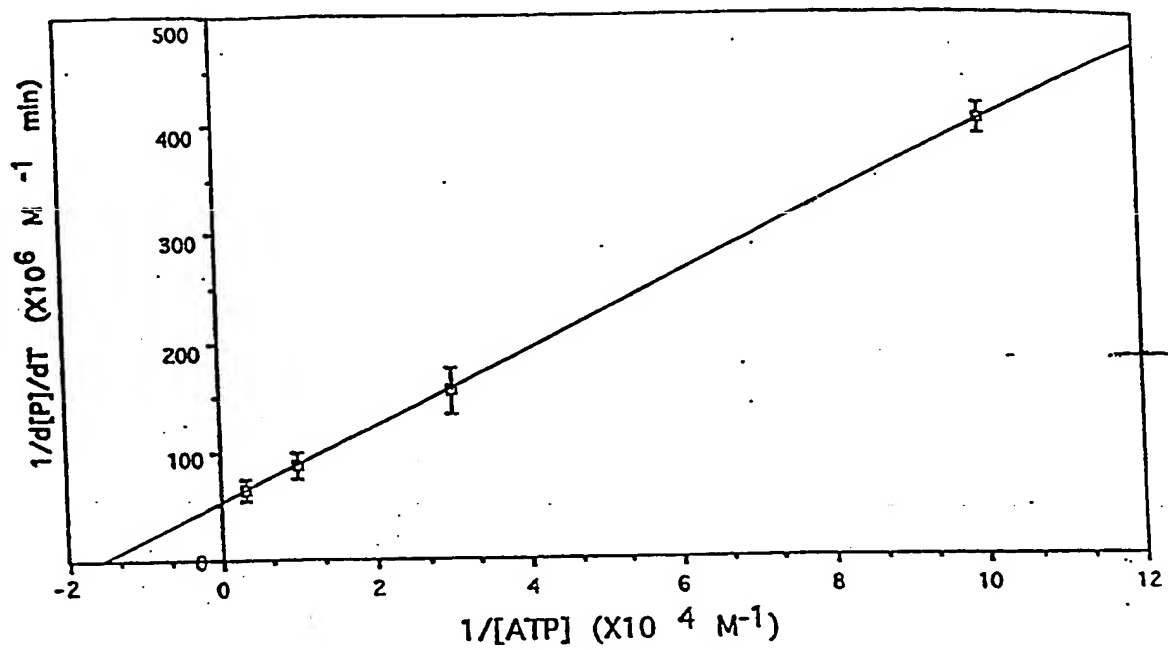


FIGURE 5B

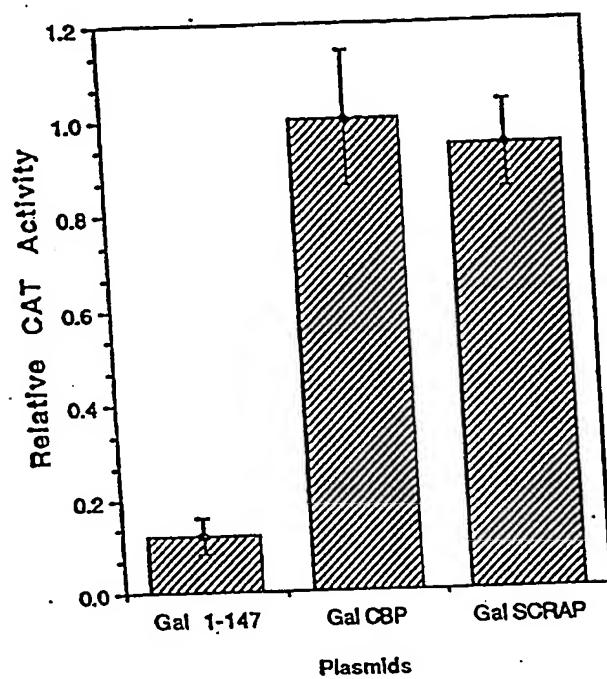


FIGURE 6

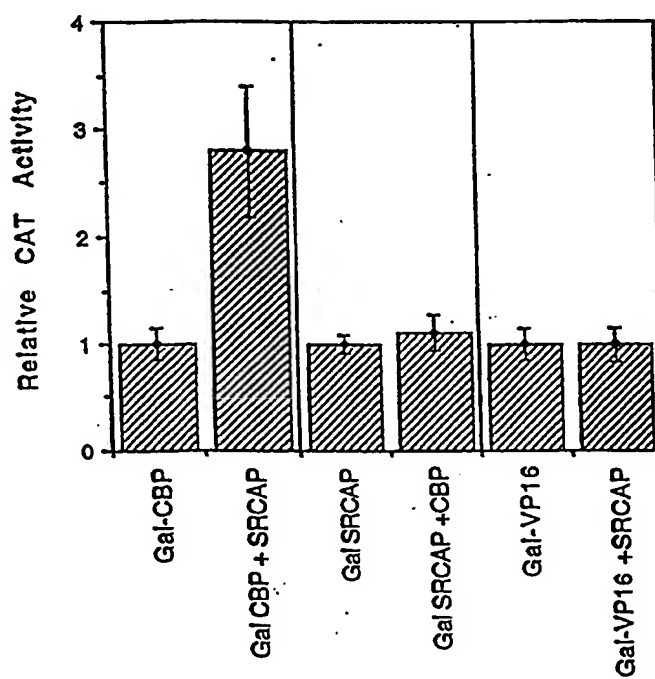


FIGURE 7

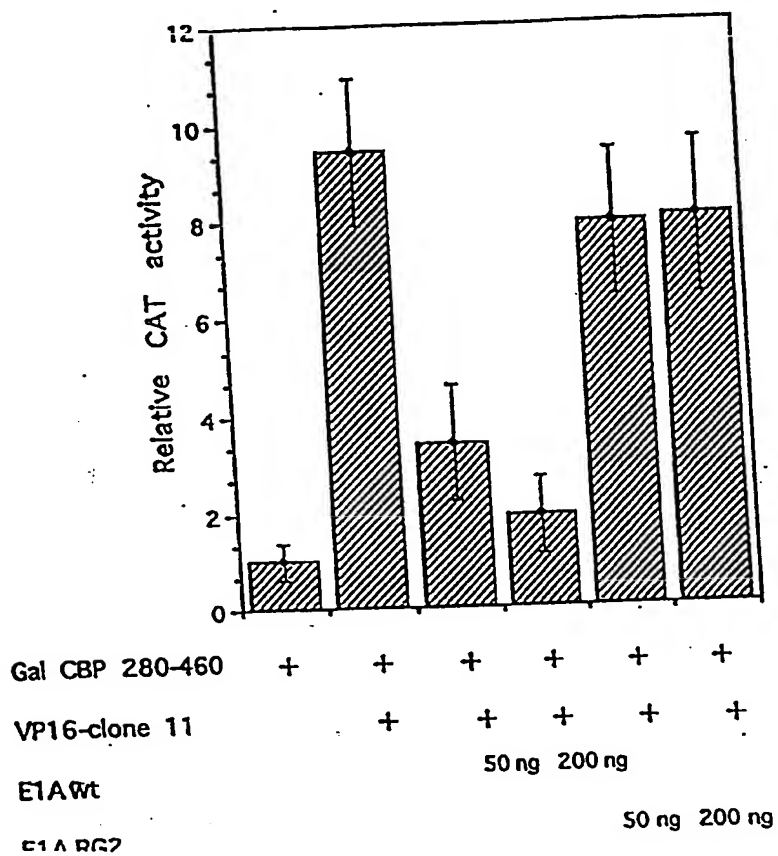


FIGURE 8

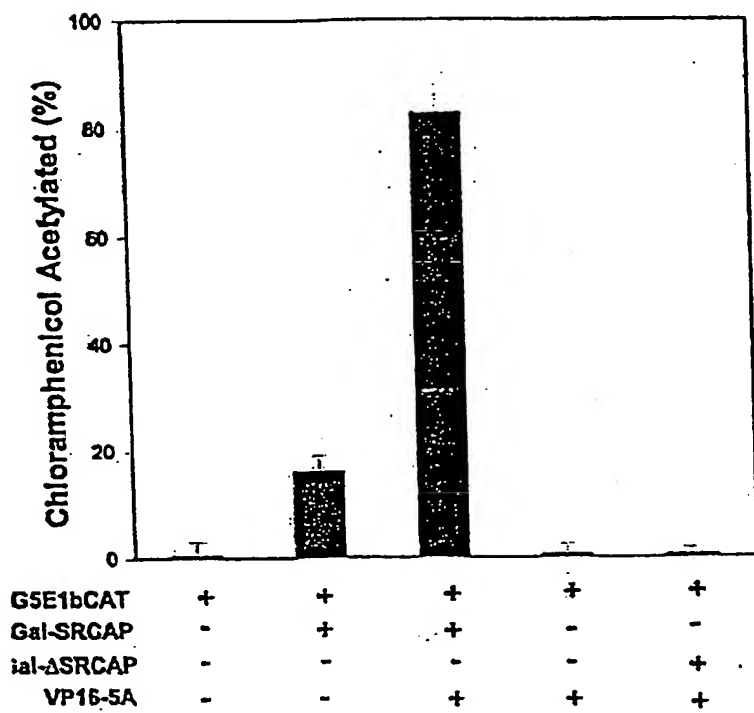


FIGURE 9

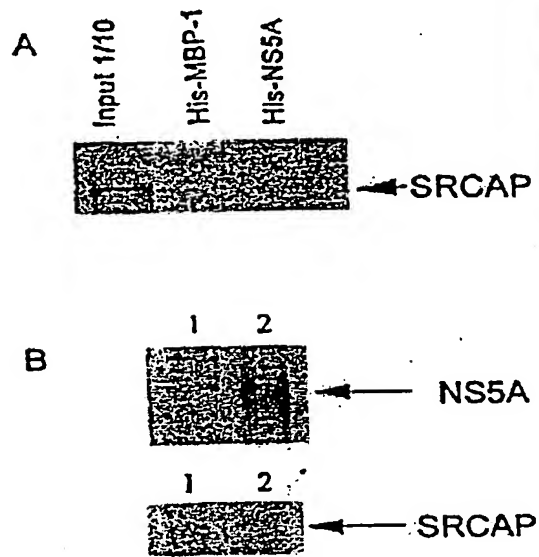


FIGURE 10



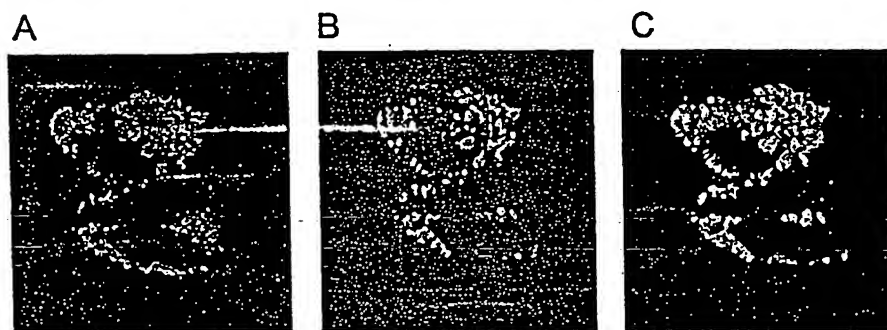


FIGURE 11

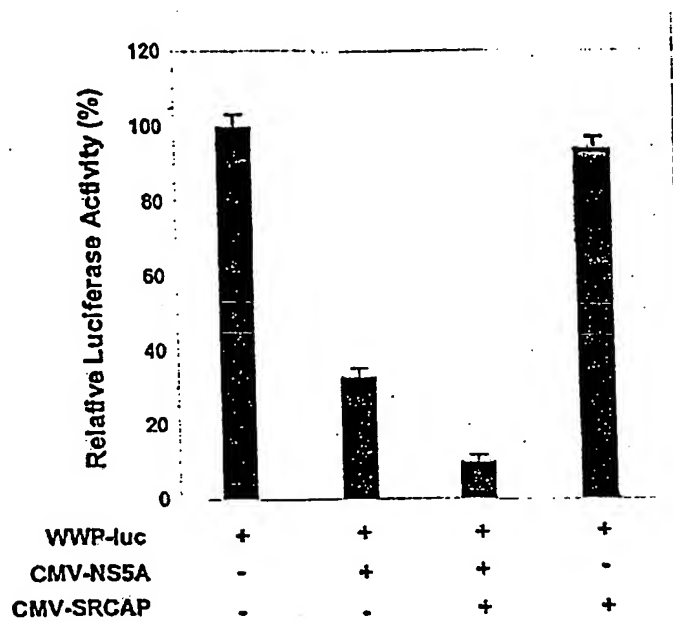
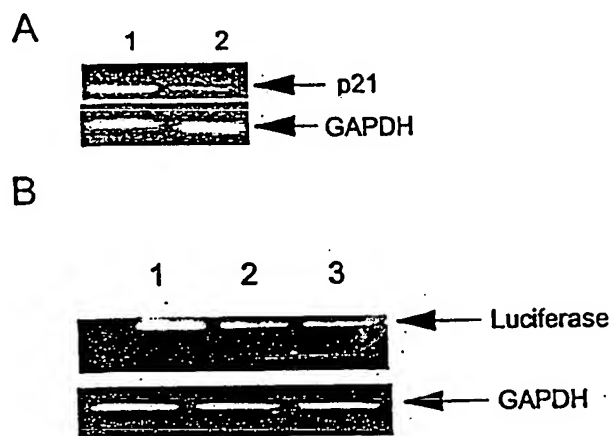


FIGURE 12

**FIGURE 13**

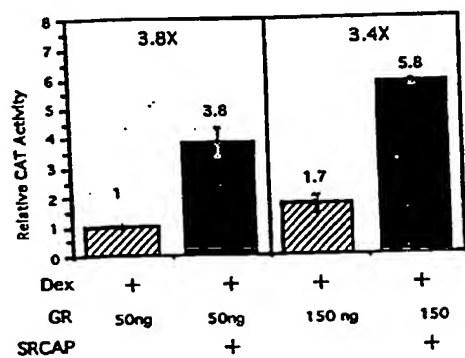


FIGURE 14

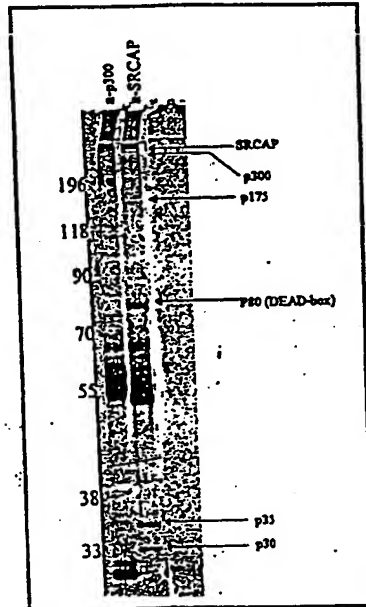


FIGURE 15

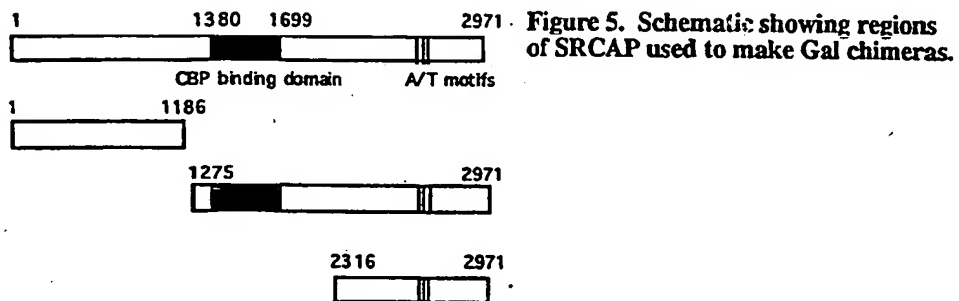


FIGURE 16

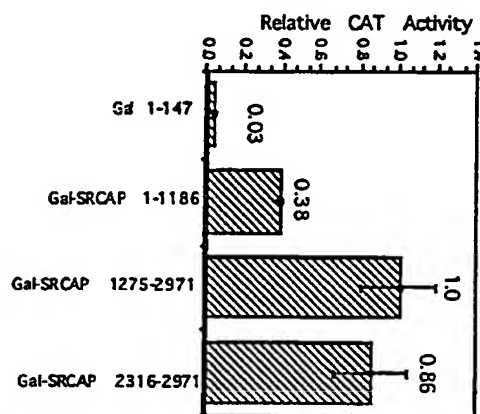


FIGURE 17

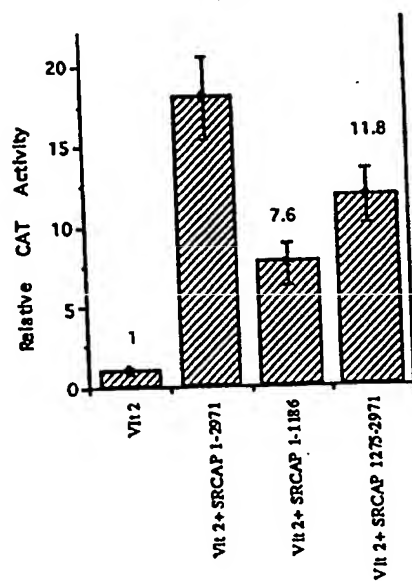


FIGURE 18



## SEQUENCE LISTING

<110> Saint Louis University  
 Chrivia, John  
 Yaciuk, Peter

<120> SNF2 Related CBP Activator Protein (SRCAP)

<130> 16153-4852

<140>

<141>

<150>

<151> 2000-05-25

<150> 60/136,620

<151> 1999-05-27

<160> 17

<170> PatentIn Ver. 2.0

<210> 1

<211> 3118

<212> PRT

<213> Human

<400> 1

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Asn	Lys	Gly	Pro	Lys	Trp	Glu	Lys	Ser	His	Ala	Glu	Ile	Ala	Glu	Gln	35	40	45	
Ala	Lys	His	Glu	Ala	Glu	Ile	Glu	Thr	Arg	Ile	Ala	Glu	Leu	Arg	Lys	50	55	60	
Glu	Gly	Phe	Trp	Ser	Leu	Lys	Arg	Leu	Pro	Lys	Val	Pro	Glu	Pro	Pro	65	70	75	80
Arg	Pro	Lys	Gly	His	Trp	Asp	Tyr	Leu	Cys	Glu	Glu	Met	Gln	Trp	Leu	85	90	95	
Ser	Ala	Asp	Phe	Ala	Gln	Glu	Arg	Arg	Trp	Lys	Arg	Gly	Val	Ala	Arg	100	105	110	
Lys	Val	Val	Arg	Met	Val	Ile	Arg	His	His	Glu	Glu	Gln	Arg	Gln	Lys	115	120	125	
Glu	Glu	Arg	Ala	Arg	Arg	Glu	Glu	Gln	Ala	Lys	Leu	Arg	Arg	Ile	Ala	130	135	140	
Ser	Thr	Met	Ala	Lys	Asp	Val	Arg	Gln	Phe	Trp	Ser	Asn	Val	Glu	Lys	145	150	155	160
Val	Val	Gln	Phe	Lys	Gln	Gln	Ser	Arg	Leu	Glu	Glu	Lys	Arg	Lys	Lys	165	170	175	
Ala	Leu	Asp	Leu	His	Leu	Asp	Phe	Ile	Val	Gly	Gln	Thr	Glu	Lys	Tyr	180	185	190	

Ser Asp Leu Leu Ser Gln Ser Leu Asn Gln Pro Leu Thr Ser Ser Lys  
 195 200 205  
 Ala Gly Ser Ser Pro Cys Leu Gly Ser Ser Ser Ala Ala Ser Ser Pro  
 210 215 220  
 Pro Pro Pro Ala Ser Arg Leu Asp Asp Glu Asp Gly Asp Phe Gln Pro  
 225 230 235 240  
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 245 250 255  
 Gln Gln Glu Gly Asn Asp Ala Glu Ala Gln Arg Arg Glu Ile Glu Leu  
 260 265 270  
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 275 280 285  
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 Ser Ser Pro Cys Leu Gly Ser Ser Ser Ala Ala Ser Ser Pro Pro Pro  
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 Pro Ala Ser Arg Leu Asp Asp Glu Asp Gly Asp Phe Gln Pro Gln Glu  
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 Asp Glu Glu Glu Asp Asp Glu Glu Thr Ile Glu Val Glu Glu Gln Gln  
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 Glu Gly Asn Asp Ala Glu Ala Gln Arg Arg Glu Ile Glu Leu Leu Arg  
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# INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/14719

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/52 C12N15/62 C12N15/11 C12N5/10 C12N9/14  
C07K16/40 G01N33/50 G01N33/566 C12Q1/68 A61K38/46

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K G01N C12Q A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

STRAND, BIOSIS

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE GENBANK 'Online! Accession No AB002307, 13 February 1999 (1999-02-13) NAGASE T.: "H. sapiens KIAA0309" XP002148212 compare nt 4026-898916 of seq. ID 11 and nt118-5008 of KIAA0309, and aa 1346-2971 of seq. 1 and aa 43-1668 of KIAA0309 &amp; NAGASE T. ET AL.: "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro." DNA RES., vol. 4, 1997, pages 141-150, the whole document</p> <p style="text-align: center;">--- -/--</p>	<p>3-7, 13-15, 17-22</p>



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Patent family members are listed in annex.

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- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
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Date of the actual completion of the international search

25 September 2000

Date of mailing of the international search report

06/10/2000

Name and mailing address of the ISA

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# INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/14719

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	<p>JOHNSTON H. ET AL.: "Identification of a novel SNF2/SWI2 protein family member, SRCAP, which interacts with CREB-Binding Protein."</p> <p>J. BIOL. CHEM., vol. 274, no. 23, 4 June 1999 (1999-06-04), pages 16370-16376, XP002148210 the whole document</p>	1-65
A	<p>LIANG G. &amp; HAI T.: "Characterization of human Activating Transcription Factor 4, a transcriptional activator that interacts with multiple domains of cAMP-responsive element-binding protein (CREB)-binding protein (CBP)."</p> <p>J. BIOL. CHEM., vol. 272, no. 38, 19 September 1997 (1997-09-19), pages 24088-24095, XP002148211 the whole document</p>	1-65